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AF13739 Nephrosel
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AF13739 Nephrosel
AF220067 Drosophil
AC015209 Drosophil
AC007475 Drosophil
AE0043823 Drosophil
L48441 Echinochloa
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AF003953 Leptospira
U94974 Leptospira
U94975 Leptospira
U94977 Leptospira
U94978 Leptospira
U94978 Leptospira
AB007012 Spirochae
AB0336 Arabidopsis
AC003000 Arabidopsis
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                                                                                                                      March 27, 2001, 08:16:52 ; Search time 2286.42 Seconds
(without alignments)
49.243 Million cell updates/sec
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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13-0CT-1997

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AB007014 354 bp DNA BCT
Spirochaeta sp. 16S rRNA gene, partial sequence.
AB007014
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AF003953
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                                                                                                                                                                                                      273136 S.cerevisia
U40812 Strongyloce
U41016 Caenorhabdi
U41545 Caenorhabdi
AL049803 Arabidops
AC083790 Homo sapi
AC036233 Homo sapi
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ACO21015 Homo sapi
ACO23155 Homo sapi
AF175672 Unculture
AF271231 Albugo ca
AF7018567 Unidentif
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Homo sapi
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AC003114 Arabidops
AB008265 Arabidops
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AL078470 Arabidops
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Adler, B., Chappel, R.J., Baranton, G., Bulach, D.M.,
Billinghurst, M.L., Letocart, M., Merien, F., Serrano, M.S. and
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Leptospira fainei 16S ribosomal RNA gene, partial sequence.
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/organism="Leptospira fainei"
/strain="Hurstbridge"
/db_xref="taxon:48782"
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335 c 439 g 314 t
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RESULT

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Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
Bacteria; Spirochaetales; Cinco,M., Smythe,L.D., Symonds,M.,
Woo,T.H.S., Patel,B.K.C., Cinco,M., Smythe,L.D., Symonds,M.,
Noris,M. and Dohnt,M.
Identification of Leptonema by real-time homogeneous assay of rapid
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Leptospira interrogans strain 48/95 16S ribosomal RNA gene, partial
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Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun
Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Sacilty of
Shin, Laboratory of Marine Molecular Microbiology, Faculty of
Agriculture, Kyoto University; Olwakecho, Kitashirakawa, Sakyoku,
Kyoto, Kyoto 306-01, Japan (E-mail:misun@kais.kyoto-u.ac.jp,
Tel:075-753-6224, Fax:075-753-6226)
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Shin, Yoshinaga, I., Uchida, A. and Ishida, Y.
Shin, M., Yoshinaga, I., Uchida, A. and Ishida, Y.
Shin, M., Yoshinaga, I., Uchida, A. and Ishida, Y.
Shin, M., Yoshinaga, I., Uchida, A. and Ishidane Oligotrophs isolated from the northern basin of Lake Biwa Oligotrophs isolated from the northern basin of Lake Biwa (Mesotrophic Lake)
Unpublished (1997)
I. and M. and
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Unpublished
2. (Dases 1 to 283)
Woo, T.H.S. Patel, B.K.C., Cinco, M., Smythe, L.D., Symonds, M., Poor, T.H.S. Patel, B.K.C., Cinco, M., Smythe, L.D., Symonds, M., Norris, M. and Dohnt, M.
Bulrect Submission
Submitted (14-May-1997) School of Science, Griffith Universitisbane, QLD 4111, Australia
                                                                   Spirochaeta sp. (sub_species:Freshwater obligate oligotroph, strain:F0-95) DNA.
Spirochaeta Sp.
Bacteria: Spirochaetales; Spirochaetaceae; Spirochaeta.
1 (bases 1 to 354)
Shin,M.-S.
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/db_xref="taxon:28185"
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1. 283
7. Coganism="Leptospira interrogans"
/strain="48/95"
/db_xref="taxon:173"
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Pred. No. 25;
0; Mismatches
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/strain="FO-95"
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Best Local Similarity 95.5%;
Matches 21; Conservative (
AB007014.1 GI:2516255
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Query Match 85.5%;
Best Local Similarity 90.9%;
Matches 20; Conservative
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90.9%;

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Best Local Similarity 90.9
Matches 20; Conservative
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1 (bases 1 to 288)

Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Science, Griffith University,
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1 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
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Leptcospira inadai 16S ribosomal RNA gene, partial sequence.
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Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct Submission Submission
Submitted (24-WAR-1997) School of Science, Griffith Unive
Brisbane, QLD 4111, Australia
Location/Qualiflers
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0; Mismatches 2;
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Pred. No. 1.4e+02;
0; Mismatches 2;
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/strain="79/95"
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Leptospira inadai 16S
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90.9%;
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Best Local Similarity 90.9%;
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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Leptospira inadal
Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
1 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadal by continuously monitoring
fluorescence during rapid cycle PCR
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                                                                                      of Science, Griffith University
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Leptcspira inadai 16s ribosomal RNA gene, partial sequence.
U94977
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2 (bases 1 to 288)

Noo.T.H.S., Smythe, L.D., Symonds, M., Norris, M., Dohnt, M., Brenner, D.J. and Patel, B.K.C.

Brenner, D.J. and Patel, B.K.C.

Direct, Submission

Submitted (24 MAR-1997) School of Science, Griffith University Brisbane, QLD 4111, Australia

Location/Qualifiers

1. 288

1. 288

1. 288

Acganism="Leptospira inadai"

/ Strain-186/94"
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Leptospira inadai 16s ribosomal RNA gene, partial sequence.
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Woo, T.H.S., Smythe, L.D., Symonds, M., Norris, M., Dohnt, M.,
Brenner, D.J. and Patel, B.K.C.
Direct Submission
Submitsed (24-MAR-1997) School of Science, Griffith Univer
Brisbane, QLD 4111, Australia
Location/Qualifiers
1. 288
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Pred. No. 1.4e+02;
); Mismatches 2;
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Pred. No. 1.4e+02;
0;. Mismatches 2;
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/organism="Leptospira inadai"
/strain="346/95"
/db_xref="taxon:29506"
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Unpublished (1997)
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Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
1 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
Fluorescence during rapid cycle PCR
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1 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadal by continuously monitoring
fluorescence during rapid cycle PCR
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Leptospira inadai 16S ribosomal RNA gene, partial sequence.
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Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct Submission
Submitted (24-MAR-1997) School of Science, Griffith Unive
Brisbane, QLD 4111, Australia
Location/Outlifers
1. 288
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/strain="268/95"
/db_xref="taxon:29506"
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Direct Submission
Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun
Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun
Shin, Laboratory of Marine Molecular Microbiology, Faculty of
Agriculture, Kyoto University; Olwakecho, Kitashirakawa, Sakyoku,
Kyoto, Kyoto 306-01, Japan (E-mail:misun@kais.kyoto-u.ac.jp,
Tel:075-753-6224, Fax:075-753-6226)
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Woo,T H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Woo,T H.S., and Patel,B.K.C.
Brenner,D.J. and Patel,B.K.C.
Direct Submission
Submitted (24-mR-1997) School of Science, Griffith University,
Brisbane, QLD 4111, Australia
Location/Qualifiers
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                                                                                                                                                                                                                                               Woo, T. H.S., Smythe, L.D., Symonds, M., Norris, M., Dohnt, M., Brenner, D.J. and Patel, B.K.C. Identification of Leptospira inadai by continuously monitoring fluorescence during rapid cycle PCR Unpublished
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                01-JAN-1998
sequence.
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Spirochaeta sp. (sub_species:Freshwater obligate oligotroph,
strain:So-104) DNA.
Spirochaeta sp.
Bacteria; Spirochaetales; Spirochaeta.
1 (bases 1 to 353)
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                      Leptospira inadai
Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
1 (bases 1 to 288)
LIU94979 288 bp DNA BCT
Leptospira inadai 16S ribosomal RNA gene, partial
U94979
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Spirochaeta sp. 16S rRNA gene, partial sequence.
ABO07012
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/organism="Leptospira inadai"
/strain="1078 VRI"
/db_xref="taxon:29506"
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<1. .>288
/product="16S ribosomal
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90.9%;
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Best Local Similarity 90.9
Matches 20; Conservative
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://www.cbs.dtu.dk/services/NetGenee/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, that are predicted by two corners without protein or EST similarity, that are predicted by two annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Simple repeats were identified by repeatmasker (Arian Smit, http://genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.
                                                                                                                                                                              Bukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eddicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 72590)

Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M., Koo, H., Moffat, K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:2642152. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TiGR web site (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence and analysis of chromosome 2 of the plant Arabidopsis
Arabidopsis thaliana chromosome II section 214 of 255 of the complete sequence. Sequence from clones T517. AC003000 AE002093
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/organism="Arabidopsis thaliana"
/cultivar="Columbia"
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Arabidopsis thaliana cDNA to mRNA.
Arabidopsis thaliana
Bukaryota: Varidiplantae: Embryophyta: Tracheophyta: Spermatophyta;
Magnoliophyta: eudicotyledons; core eudicots: Rosidae: eurosids II:
Brassicales: Brassicaceae; Arabidopsis.
1 (bases 1 to 1012)
1 (bases 1 to 1012)
Green, P.J.
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TUVLYQAGYYASNSEKYPLGGTYTALQNAFHTTPEVYCKRDAIDEIRICFYKDFKPRD
CVGSODLTSRKSCPKYVSLPFYTPLGGEAMVLKMPTEREAL"
197 c 117 g 311 t
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Arabidopsis thaliana ribonuclease (RNS2) mRNA, complete cds.
M98336
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Proc. Natl. Acad. Sci. U.S.A. 90 (11), 5118-5122 (1993)
93281708
                                                                                                     /sub_species="Freshwater obligate oligotroph"
/db_xref="taxon:28185"
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                  /organism="Spirochaeta sp."/strain="SO-104"
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/db_xref="GI:289210"
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/product="ribonuclease"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="RNS2"
16. .795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="RNS2"
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20; Conserv
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Best Local S
Matches 20
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ORIGIN
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ORIGIN
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MEDLINE
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AC003000
LOCUS
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SOURCE
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FEATURES
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CDS

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KGKMCCLEINDLDAGAGRAGGTTOYTVNNOMVNATLANIADNPTNVOLPGKYNKEENA
RVPIICTGNDFSTLXAPLIRDGRMEKFYWAPTREDRIGVCKGIFFTDKIKDEDIVTLV
DOEPGOSDIDFFGALRARVYDEFVRFVESLGVEKIGKRLVNSREGPPVFEQPEMTYEK
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COMPIEMENT (17561. 17639)
//rpt_family="(17A)"
//origin(-148783. 18921.19188. 19352,19496. 19674,19766. 19861,
19965. 20034,20131. 20261,20593. >>21237)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="T517.4; predicted by genscan"
join(1878: 18921,19188. .19352,19496. .19674,19766. .19861,
19965. .20034,20131. .20261,20593. .21237)
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//gene="At2g39750"
complement(21380. .>24814)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                               KGKWCCLFINDLDGGAGRWGGTTOTTVNNOWNNATLANITADNFTNVOLPGANNKEENA
RVPIICTGNDFSTLYAPLIRDGRMEKFYWAPTREDRIGVCKGIFRTDKIKDEDIVTLV
BOPFGOSIDFFCALRARVYDEVRKFYESLGVFKIGKRLVNSREGPPVFEQPEMTYEK
LMFYGNMLVMSDENKRYOLLAFTLSQAALGDANADAIGFFTGKGRQQVNLPVPEG
CTDPVARNFEDFTAKSDGGTCVYNF"
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GTHHAYLSSTRYSQGLRQYNLDNMMGFFIAPAFMDKLVVHITKNFTTLPNIKVPLI
AQSNKKSNGSFKVLAVKEDKQTDGDRWRGLAYDTSDDQQDITRGKGMVDSVFQAPMGT
GTHHAVLSSYEXVSQGLRQYNLDNMMDGFYIAPAFMDKLVVHITKNFLTLPNIKVPLI
LGIWGGKGOGKSFQCELVMAKMGINPIMMSAGELESGNAGEPAKLIRQRYREAADLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                           LGIWGGKGQGKSFQCELVMAKMGINPIMMSAGELESGNAGEPAKLIRQRYREAADLIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85;
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0; Mismatches
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                      /codon_start=]
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90.9%;
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Best Local Similarity
Matches 20; Conserv
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SOURCE
ORGANISM
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AF165146
LOCUS
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SAAAPSSDVVSEGLDRSAFQMYYDDGTDSGLRPLPPSMTEFLLGSGFDRLLDQISQIE
LNTNRNLRSCEHPPASKSAFLBALPLIELEIDPTHLLSDSQSHCAVCKENFVLKSSAREMP
CNHIYHPDCTLPWLA RNSCPVCRHELPAEDLTDGTGAALTAVTATREEEEDSAAGLT
IWRLPGGGFAVGRIPGGGWRGDDRMPVYTEVDGGRLGDERLPRRVAMGSRRGGRDG
GSRERGGGFAGRIMRLFGCFSGSSGSIAAAAASSGSGSRIRVTRRTRSFSMFSTASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="WOSSSSSLSKNFLRISVLLIFPLTFCKTSSTNOTLLFSLK
TQKLPQSSDKLSFRHNVTLYTLAVGDPPQNISMVLDTGSELSWHJCKKSPNLGSVF
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FVIGSYTRPGTLEGGNBSGLSSNSEEDAKSTGLMGMNRGSLSFVNQLGFSKFSKISS
SDSSGFLLLGDASYSWLGPIQYTPLVLQSTPLPYFPRNAYTVQLEGTRVGSKILSLPK
SVFVPDHGTAGGQTMVDSGTPFLWGWYTALKNFFITQTKSVLRUVDDPDFVFQGTM
DLCKKVGSTTRRPFSGLPWYSLMFRGAEMSVSGQKLLYRVNGAGSGCKEEVYCFTFGN
SDLLGIEAFVIGHHQQNVWMFFDLAKSRVGFAGNVCCDLASQRLGIRD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="TSI7.3"
13364. .13461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(13323. .13599,13713. .14005,14087. .14559,
14651. .14736,14836. .14941,15033. .15349,15834. .16055))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="poly_a"---,
complement(join13323. .13599,13724. .14005,14087. .14559,
14651. .14736,14636. .14941,15033. .15349,15834. .16055))
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                                                                                                                                                                                                                                                                                                                                                                                        /note="T517.1; similar to
GP|2245012|qn1|prD|e327000|297341"
complement(4584 . 5909)
/gene="At2g39710"
                                                                                     'note="Sequence from clone T517"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Rubisco activase"
/protein_id="AABB7122.1"
/db_xref="GI:2642155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(<10039. .11304)
/gene="At2g39720"
complement(<10039. .11304)
/gene="At2g39720"
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/gene="At2g39720"
/note="unknown protein"
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/gene="At2g39730"
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                                                                                                                                                                                                                                               /rpt_family="POLY_A"
complement(<4584. .>5909)
/gene="At2939110"
                                                                                                                                                                                                                                                                                                                                          complement(<4584. .>5909)
/gene="At2g39710"
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complement(1000..1024)
/rpt_family="POLY_A"
                                                                                                                                                                                                 complement(1266..1291)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:2642154"
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CDS

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/translation="makkSmiereskraalvakyatrroalkaaloktkSfderlulo
HQLQDLPVNSVPCRLHNRCTITGRPKGYYRDFGLSRHELRAMAHGCLLPGVTRASW"
  The complete chloroplast DNA sequence of the green alga
Nephroselmis olivacea: insights into the architecture of ancestral
                                                                                                2 (bases 1 to 200799)
Turmel,M., Otis,C. and Lemieux,C.
Direct Submission
Submitted (24-MAR-1999) Biochimie, Universite Laval, Pavillon Charles Eugene Marchand, Quebec GIK 7P4, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="M protein of photosystem II"
/protein_id="AbA779.1"
/db.xref="GI:5880666"
/translation="MEVNILGLIATALFIIIPTSFLLLLYVKTASOON"
                                            chloroplast genomes
Proc. Natl. Acad. Sci. U.S.A. 96 (18), 10248-10253 (1999)
99398694
                                                                                                                                                                                                                                                                                                                         ....92126
/note="Region: large single-copy region (LSC)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'anticodon=(pos:1136. .1138, aa:Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /anticodon=(pos:1652. .1654, aa:Met)
                                                                                                                                                                                                                        /anticodon=(pos:798. .800,aa:Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="ribosomal protein S14"
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/db_xref="G1:5880685"
                                                                                                                                                                                                                                                                                                                                                                                                           /note="codons recognized: CUY" /product="tRNA-Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="codons recognized: CAR"
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/codon_start=1
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/qene="trnL(uaq)"
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/gene="trnL(uag)"
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/gene="trnM(cau)"
1733. .3862
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332. .634
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Schudy, A., Blechschmidt, K., Schillhabel, M., Baumgart, C., Menzel, U., Weber, J., Schattevoy, R. and Rosenthal, A.
Direct Submission
Submitted (06-3UL-1999) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
Genome Sequencing Center Jena.
Direct Submission
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 109723)
Schudy,A., Blechschmidt,K., Menzel,U., Polley,A., Reichwald,K., Rump,A., Schilnabel,M.B., Taudien,S., Wen,G., Schlegelberger,B., Siebert,R. and Rosenthal,A.
                                                                                                                                                                                                                                                                                                                             Submitted (24-MAY-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11. Jena 07745, Germany on Jun 1, 2000 this sequence version replaced gl:5514637.

* NOTE: This is a "working draft" sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
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Nephroselmis olivacea chloroplast DNA, complete genome.
AF137379
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Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
Chlorodendrales; Chlorodendraceae; Nephroselmis.
I (bases 1 to 200799)
Turmel, M., Otis, C. and Lemieux, C.
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90.9%; Pred. No. 82;
ive 0; Mismatches 2;
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22757 c 23188 g 31709 t
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clone_end:SP6
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KEGIGKDEAQQIKQDEEGAFTVTVK"
complement(9442..9846)
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KPGYLTRNPLKERKKYGLKKARKAPQFSKR"
complement(9998. .11485)
AVPAGLLTVPFIESINKFQNPFRRPVATTVFLIGTVVAIWLGIGATLPIDISLTLGLF
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The complete chloroplast DNA sequence of the green alga
Nephroselmis olivacea: insights into the architecture of ancestral
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Proc. Natl: Acad. Sci. U.S.A. 96 (18), 10248-10253 (1999)
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Nephroselmis olivacea chloroplast DNA, complete genome.
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Bukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
Chlorodendrales; Chlorodendraceae; Nephroselmis.
1 (bases 1 to 200799)
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90.9%; Pred. No. 77;
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complement(9045, 9431)
/gene="rpl12"
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/gene="rps9"
                                                                                                                .8779)
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                                                                                   /gene="petB"
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KEYWORDS
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                                                               gene
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Direct Submission
Submitted (24-MAR-1999) Biochimie, Universite Laval, Pavillon
Charles-Eugene Marchand, Quebec G1K 7P4, Canada
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"M protein of photosystem II"
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Search completed: March 27, 2001, 08:17:03 Job time: 5900 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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U60594 Leptospira

Description

SUMMARIES

Leptospira L.wolbachii

Leptospira

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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1 (bases 1 to 1450)
Petersen,A.M., Krogfelt,K.A., Perolat,P., Boye,K. and Schlichting,P.
Leptospira fainei serovar Hurstbridge isolated from two patients with Weil's syndrome
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//gene"16S rRNA"
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16S ribosomal RNA; 16S rRNA gene
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Direct Submission
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/ organism="Leptospira interrogans"
/ strain="serovar canicola strain Mov/db_xref="taxon:173"
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Leptospira interrogans.
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Bacteria; Spirochaetales;
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Fukunaga,M.
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rRNA gene, partial
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Lgggagaggcaagtggaattccaggtgtagcggtgaaatgcgtagatatctggaggaaca
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Leptospira weilii
Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
1 (bases 1 to 1480)
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Direct Submission
Submitted (09-FEB-1993) Hookey J.V., Public Health Laboratory
Service, Leptospira Reference Laboratory, Stonebow Road, Hereford,
Herefordshire, United Kingdom, HRI 2ER
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1 (bases 1 to 1374)
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2; Mismatches 4
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/strain="LYME"
/db_xref="taxon:29506"
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Submitted (25-UUL-1994) Michael McClelland, California Institute
Biological Research, 11099 North Torrey Pines Road, La Jolla, CA
92037, USA
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Ralph,D. and McClelland,M. Phylogenetic evidence for horizontal transfer of an intervening Phylogenetic evidence for horizontal transfer of an intervening sequence between species in a spirochete genus J. Bacteriol. 176 (19), 5882-5987 (1994)
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Pred. No. 1.7e-13;
0; Mismatches 80; Indels
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/strain="serogroup Celledoni, serovar
Celledoni (ATCC 43285)"
/isolate="WA45"
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McClelland, M.
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Ralph, D. and McClelland, M. Phylogenetic evidence for horizontal transfer of sequence between species in a spirochete genus J. Bacteriol. (1994) In press 2 (bases 1 to 1489)
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       and, California
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                                   /organism="Leptospira weilli"
/strain="serogroup Hebdomadis, subserogroup
serovar worsfoldi, strain Worsfold"
/isolate="WA52"
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Leptospira borgpetersenii Hardjo bovis/Sponselee 16S rRNA gene,
partial sequence.
U12670 GI:558929
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taccagtigitgggggttttaaccctcagtaacgaacctaacggattaagtagaccgcct
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Submitted (25-JUL-1994) Michael McClelland, California
Biological Research, 11099 North Torrey Pines Road, La
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Leptospira borgpetersenii
Bacteria: Spirochaetales; Leptospiraceae; Leptospira.
I (bases 1 to 1513)
Ralph.D. and McClelland,M.
Phylogenetic evidence for horizontal transfer of an isequence between species in a spirochete genus
J. Bacteriol. (1994) In press
McClelland,M.
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                                           Score 1262.2; DB
Pred. No. 1.8e-13;
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/organism="Leptospira borg.
/strain="serovar hardjo, s'/isolate="BDS0"
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<1. .1513
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                      /product="16S rRNA"
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Best Local Similarity 94.0%;
Matches 1375; Conservative
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borgpetersenii 1627 Burgas 165 rRNA gene, partial
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/strain="sercoar balcanica, strain 1627 Burgas"
/isolate="BD30"
/db_xref="taxon:174"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (25-JUL-1994) Michael McClelland, California
Biological Research, 11099 North Torrey Pines Road, La
92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leptospira borgpetersenii.
Leptospira borgpetersenii
Bacteria: Spirochaetales; Leptospiraceae; Leptospira.
1 (bases 1 to 1489)
Ralph,D. and McClelland,M.
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sequence between species in a spirochete genus
J. Bacteriol. 176 (19), 5982-5987 (1994)
95014031
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Score 1260.8; DB Pred. No. 1.9e-13;
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Biological Research, 11099
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McClelland, M.
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Pred. No. 1.9e-13;
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ot Michael McClelland, California Institute 199 North Torrey Pines Road, La Jolla, CA 1317 Bragg 1197 1257 1272 an intervening 18-FEB-1995 partial sequence cta-ccttaagttgggcactggtacgaaactgccggtgacaaaccggaggaaggcgggga ggggtctgcaactcgaccccatgaagtcggaatcgctagtaatcgcggatcagcatgccg cggtgaatacgttcccggaccttgtacacaccgcccgtcacaccacctgagtggggagca Fort Length 1516; /strain="serogroup Autumnalis, subserogroup serover fortbragg, strain Fort Bragg" /isolate="NB36" Leptospira oţ Ralph, D. and McClelland, M.
Phylogenetic evidence for horizontal transfer c
sequence between species in a spirochete genus
J. Bacteriol. 176 (19), 5982-5987 (1994) gene, 5 Bacteria; Spirochaetales; Leptospiracéae; 1 (bases 1 to 1516) 1. .1516 /organism="Leptospira noguchii" rRNA

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                             tgacgicaaaiccicaiggccittaigiccagggccacacacgigctacaaiggccgaia
                                                           cagagggtcgccaactcgcaagagggagctaatctctaaaagtcggtcccagttcggatt
                                                                  DB 2; Length 1425
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ilarity 94.2%; Pred. No. 2.5e-13;
Conservative 2; Mismatches 76;
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for 16S 1
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Leptospira borgpetersenii
Bacteria; Spirochaetales;
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Biological Research, 11099 North Torrey Pines Road, La Jolla, CA
92037, USA
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Sarmin, serovar sarmin, strain Sarmin"
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Submitted (09-FEB-1993) Hookey J.V., Public Health
Service, Leptospira Reference Laboratory, Stonebow
Herefordshire, United Kingdom, HRI 2ER
Location/Qualifiers
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/strain="CYNOPTERI 3522 C"
/db_xref="taxon:29507"
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Pred. No. 3.4e-13;
3; Mismatches 76;
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Institute Jolla, CA

Direct Submission Submitted (25-JUL-1994) Michael McClelland, California Biological Research, 11099 North Torrey Pines Road, La

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Location/Qualifiers 1. .1494 /organism="Leptospira

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jo

Phylogenetic evidence for horizontal transfer c sequence between species in a spirochete genus J Bacteriol. 176 (19), 5982-5987 (1994) 95014031

(bases 1 to 1494)

McClelland, M.

Bacteria, Spirochaetales, Leptospiraceae, 1 (bases 1 to 1494) Ralph, D. and McClelland, M.

Leptospira santarosai Leptospira santarosai

GI:558931

U12672 U12672.1

Leptospira

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                                                                                                                 7 ;
                                                                                                Length 1494;
/strain="serogroup Tarassovi, subserogroup / serovar atlantae, strain LT81" /isolate="sa39" / db_xref="taxon:28183" / 1.1494
                                                             others
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Pred. No. 4.1e-13;
0; Mismatches 92;
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                                               /product="16S
332 c 4
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Best Local Similarity 93.2%;
Matches 1363; Conservative (
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BCT 18-FEB-1995 gene, partial sequence.

LSU12672 1494 bp DNA Leptospira santarosai LT81 16S rRNA

LOCUS DEFINITION

LSU12672

RESULT

Spirochaetes

related

to 1418)

(bases 1 to 1418)

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Phylogeny of Leptospiraceae and Unpublished
                          Hookey, J.V.
      Hookey, J.V.
                                                         source
                                                                                     BASE COUNT
ORIGIN
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  Service, Leptospira Reference Laboratory, Stonebow i Herefordshire, United Kingdom, IRI 2ER
Location/Qualifiers
1. .1418
/organia="Leptospira meyeri"
/strain="RaNaRUM ICF"
/db.xref="total"
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Pred. No. 4.6e-13;
2; Mismatches 75;
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324 c 421 q 29
Direct Submission
Submitted (09-FEB-1993) Hookey
Service, Leptospira Reference I
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ilarity 94.2%;
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02-DEC-1993

(partial)

ribosomal RNA DNA

L.ml6SRDNX 1418 bp L.meyeri gene for 16S 221648

LOCUS DEFINITION

GI:433585

221648.1

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

16S ribosomal RNA. Leptospira meyeri. Leptospira meyeri Bacteria; Spirochaetales; Leptospiraceae; Leptospira.

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rrna		Query Match Best Local Similarii Matches 1309; Conse	Qy 49 cgagcgggtac 	108	133		Qy 288 ggaactgagace 	348	Qy 408 ttaggca-ggae                Db 373 GTAAGCAGGAN	Qy 467 tacgtgccagce 	Oy 527 aaagggtgcgta 	Qy 587 tgcacttgaaac 	Qy 647 tgaaatgcgtag 	Qy 707 gacgctgaggca 	Oy 767 ctaaacgttgtc 	Oy 827 agtagaccgcct                         Db 793 AGTAGACCGCCT	Oy 887 gcacaagcggtc 	Oy 947 gacatggatctg
Oy 734 taaacgggattagataccccggtaatccacgcctaaacgttgtctaccagttgttgggg 793 	83	Oy 854 aagagtgaaactcaaaggaattgacggggtccgcacaagcggtggagcatgtggtttaa 913 	Oy 914 ttcgatgataccccaaaaacttcactgggcttgacatggatctgaatcatgtaggata 973 	10	Oy 1034 tgttgggttaagtccgcaacgagcgcaaccctatcgtatgttgctacc-ttaagttgg 1092 	Qy       1093       gcactggtacgaaactgccggtgacaaaccggaggaggaggggggatgacgtcaaatcctc       1152         D       1111	Qy 1153 atggcctttatgtccagggccacacacgtgctacaatggccgatacagagggtcgccaac 1212 	12	Oy 1273 accecatgaagteggaategctagtaategeggateagcatgeegeggtgaatacgttec 1332 	1333 eggaccttgtacacaccgccgtcacaccactgggtggggacaccgaagtgttt 139	Oy 1393 gitaaccgtaaggagacagactactaaggigaaactcgi 1431 	RESULT 15	LILSSRRN LILSSRRN 1396 bp mRNA BCT 24-AUG-1993 DEFINITION L.Interrogans 16s ribosomal RNA. VECESSION 212817 VERSTON VIPE 170 CT. 14002	21201/1 21:440V 16S ribosomal RNA; ribosomal RNA. Leptospira interrogans. Leptospira interrogans	REFERENCE 1 (bases 1 to 1396) AUTHORS Bryden,J., Gatehouse,L., Gatehouse,J.A. and Hookey,J.V. TITLE Authoristed PCR cycle sequencing of 16S ribosomal RNA genes	REFERENCE 2 (bases 1 to 1396) AUTHORS Hookey, J.V. TITLE Direct Submission	JOURNAL SUBMILLER (19-JUN-1992) NOOKEY U., FUBLIC HEBLTH LABORATORY SERVICE, LEPTOSITER REference Laboratory, Stonebow Road, Hereford, Herefordshire, United Kingdom, HR1 2ER FEATURES Location/Qualifiers 1. 1966	

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gaatcatgtagagatatatgagcettcgggcagattcacaggtgctgca 1006
                                                                                                 taactttccgaaaggaaagctaataccgatagtcctgttggatcacaag 167
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                                                              DB 2;
                                                             Score 1232.8; DB 2;
Pred. No. 5.6e-13;
0; Mismatches 72;
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a 319 c 418 g 294 t
/db_xref="taxon:173"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AR062865 Sequence A00432 Nucleotide	AX009010 Sequence AX007733 Sequence	~	A40518 Sequence 55 A88271 Sequence 41	A88273 Sequence 42 A89045 Sequence 11		I26234 Sequence 19 AX007732 Sequence	A88272 Sequence 42 A88466 Sequence 61		m	AR033480 Sequence	157664 Sequence 20
SUMMARIES	AR062865 A00432	AX009010 AX007733	AA00//34 A25812	A40518 A88271	A88273 A89045	A90238 A90240	126234 AX007732	A88272 A88466	A90239 A90433	AR033435	AR033480	157664
DB	81	79	83	81	81	81 81	81 79	81 81	81 81	81	81	81
Length DB	10	14	17.	14 14	14 14	14 14	14 15	15	15	15	15	15
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0 100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	771	<i></i>			٠ <i>د</i>	7	~ ~	~ ~	7	7	7	7
ult No.	- 77	m 4 ⊓	0 to 1	~ 8	9 01	11	13	15	17	19	50	21
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Stuyver, L. Method for detection of drug-selected mutations in the hiv protease
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Eukaryota, Metazoa, Chordata, Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 14)
Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
A method for stimulating the immune system
Patent: WO 9963975-A 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLEGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
Location/Qualifiers
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                                                                                                                                                             Length 13;
                                                                                                                                                                                        Indels

    14 / Organism="Aids-associated retrovirus"

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                                                                                                                                                          DB 81; Le
5.1e+05;
hes 0;
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INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
Location/Qualifiers
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Viruses; Retroid viruses; Retroviridae.
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                                                                                                                                                            s; Score 7; DB 8; Pred. No. 5.16 0; Mismatches
PAPILLOMAVIRUS-INDUCED TUMOURS
Patent: WO 9010459-A 7 20-SEP-1990;
Transgene S.A
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Sequence 275 from Patent W09967428.
AX007733 AX007733.1 GI:9995430
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Sequence 43 from Patent W09963975.
AX009010 GI:9996384
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/db_xref="taxon:9606"
3 c 4 9 4
                                                                      /organism="unidentified"
/db_xref="taxon:32644"
3 c 4 g
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                                           Location/Qualifiers
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Best Local Similarity 100.0%;
Matches 7; Conservative 0
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Matches 7; Conservative
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AUTHORS
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157709 Sequence 24
A97828 Sequence 15
A97828 Sequence 10
AR084439 Sequence
AR093881 Sequence
152073 Sequence 32
152073 Sequence 15
A65762 Sequence 43
A97904 Sequence 43
AR055055 Sequence
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                                                                                                                                                                         104576 Sequence 6
113562 Sequence 4
115174 Sequence 23
132561 Sequence 25
137420 Sequence 43
150672 Sequence 4
153069 Sequence 81
189345 Sequence 81
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                                                                                                                                                                                                                                                                                         Sequence 43
Nucleotide
Nucleotide
Sequence 89
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A00432.1 GI:14504
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A07301
A07302
A45212
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100.0%; Pred. No. 5.3
:ive 0; Mismatches
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Sequence 13 from patent US 5843767.
AR062865. GI:5990556
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152073
A65762
A97904
AR046017
AR053055
                                             AR084439
AR093881
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37420
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A07301
A07302
A45212
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Beattie, K.L.
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Best Local Similarity 100.
Matches 7; Conservative
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DEFINITION ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE

AR062865/c

source

JOURNAL

FEATURES

BASE COUNT

ORIGIN

DEFINITION ACCESSION

A00432/c

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ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

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AX007734/c

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JOURNAL

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ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b)) Patent: WO 9425578-A 55 10-NOV-1994; BIOGNOSTIK GES (DE)
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L (bases 1 to 14)

Brysch, W. and Schlingensiepen, K.

AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

Patent: WO 9833904-A 06-AUG-1998;

BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)

Location/Qualifiers
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A88273/c
LOCUS A88273 14 bp DNA
DEFINITION Sequence 421 from Patent W09833904.
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Sequence 419 from Patent WO9833904.
A88271
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Sequence 55 from Patent W09425578.
A40518

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/organism="unidentified"
/db_xref="taxon:32644"

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/organism="unidentified"
/db_xref="taxon:32644"
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100.0%; Score 7; DB 81; Length 14;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:11966"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent: WO 9967428-A 29-DEC-1999;
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="synthetic construct"
/db_xref="taxon:32630"
4 c 2 g 4 t
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Aids-associated retrovirus
Viruses; Retroid viruses; Retroviridae.
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                                                                                                                                                                                                                                                       AX007734 14 bp DNA
Sequence 276 from Patent W09967428.
AX007734
/db_xref="taxon:11966"
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polynucleotide 14C12
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artificial sequence.
1 (bases 1 to 14)
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Stuyver, L.
                                                                                                              Conservative
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Best Local Similarity
Matches 7; Conserv
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AUTHORS JOURNAL

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22-JAN-2000

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ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

ACCESSION VERSION KEYWORDS SOURCE

BASE COUNT ORIGIN

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[ (bases 1 to 14)]
Vergnand,G.
Vergnand,G.
Nocess for detection of new polymorphic loci in a DNA sequence, nucleotide sequences forming hybridization probes and their applications
Patent: US 5556955-A 19 17-SEP-1996;
Location/Oualifiers
                                                                                                                                                                           Query Match
100.0%; Score 7; DB 81; Length 14;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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Brysch,W.D. and Schlingensiepen,K.D.
An antisense oligonuclectide preparation method
Patent: EP 0856579-A 05-AUG-1998;
BIOGNOSTIK GES (DE)
Location/Qualifiers
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Sequence 19 from patent US 5556955.
126234
                                                    1. .14
/organism="unidentified"
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5 a 6 0 g 5
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Sequence 421 from Patent EP0856579.
A90240
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/db_xref="taxon:32644"
1 4 c 0 9
     Patent: EP 0856579-A 05-AUG-1998;
BIOGNOSTIK GES (DE)
Location/Qualifiers
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Unclassified.

L (bases 1 to 14)

B Lysch, W. and Schlingensiepen, K.

AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

PARENT: MO 9833904-A 06-AUG-1998;

BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)

Location/Qualifiers
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5e+05;
hes 0; Indels
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                                                                                                       1 (bases 1 to 14)
Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLEOTIDE PREPARATION METHOD
PATENT: WO 9833904-A 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
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Brysch,W.D. and Schlingensiepen,K.D.
An antisense oligonucleotide preparation method
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Sequence 1193 from Patent WO9833904.
AB9045.
AB9045.1 GI:6737615
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Sequence 419 from Patent EP0856579.
A90238
A90238.1 GI:6738752
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/organism="unidentified"
/db_xref="taxon:32644"
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/db_xref="taxon:32644"
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A88273
A88273.1 GI:6736843
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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AUTHORS TITLE JOURNAL

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07-0CT-1996

RESULT 11 A90238/c LOCUS DEFINITION ACCESSION VERSION

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ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

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Aids-associated retrovirus.
Aids-associated retrovirus
Viruses; Retroid viruses; Retroviridae.
1 (bases 1 to 15)
Stuyver,L.
Method for detection of drug-selected mutations in the hiv protease
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Ouery Match 100.0%; Score 7; DB 81; Length 14; Best Local Similarity 100.0%; Pred. No. 5e+05; Matches 7; Conservative 0; Mismatches 0; Indels
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1 (bases 1 to 15)

Brysch, M, and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

L Patent: WO 9833904-A 06-AUG-1998;
BIOGNOSTIK GES (DE): BRYSCH WOLFGANG (DE)
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Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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/organism="Aids-associated retrovirus"
/db_xref="taxon:11966"
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INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
Location/Qualifiers
                                                                                                                                                        AX007732 15 bp DNA
Sequence 274 from Patent WO9967428.
AX007732
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Sequence 420 from Patent W09833904.
A88272
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/organism="unidentified"
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Search completed: March 27, 2001, 08:17:04 Job time: 5901 sec

Integrin alpha 6 s Human C-raf target HIV-1 protease gen HIV-1 protease gen HIV-1 protease gen Immunosuppressant Substrate for hair Sequence of initia Sequence of initia Human CD40 hammerh Mouse B7-2 hammerh Human B7-2 hammerh Human B7-2 hammerh Human B7-2 hammerh Rabbit CETP HH rib Gene antisers ErbB-2 gene antisers FrbB-2 gene antiser Funman NR8 gene pro Human NR8 gene

us-09-380-826a-4.rng

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GenCore version right (c) 1993 - 2000 earch, using sw model 27, 2001, 08:22:58;	US-09-380-826A-4 7 1 tgttgga 7 IDENTITY_NUC Gapop 10.0 , Gapext 1.0		N_Geneseq_36:*  1: /cgn2_2/gcgdata/geneseq/g: 2: /cgn2_2/gcgdata/geneseq/g: 3: /cgn2_2/gcgdata/geneseq/g: 5: /cgn2_2/gcgdata/geneseq/g: 6: /cgn2_2/gcgdata/geneseq/g: 6: /cgn2_2/gcgdata/geneseq/g: 7: /cgn2_2/gcgdata/geneseq/g: 8: /cgn2_2/gcgdata/geneseq/g: 10: /cgn2_2/gcgdata/geneseq/g: 11: /cgn2_2/gcgdata/geneseq/g: 12: /cgn2_2/gcgdata/geneseq/g: 13: /cgn2_2/gcgdata/geneseq/g: 14: /cgn2_2/gcgdata/geneseq/g: 15: /cgn2_2/gcgdata/geneseq/g: 16: /cgn2_2/gcgdata/geneseq/g: 17: /cgn2_2/gcgdata/geneseq/g: 18: /cgn2_2/gcgdata/geneseq/g: 18: /cgn2_2/gcgdata/geneseq/g: 19: /cgn2_2/gcgdata/geneseq/g: 19: /cgn2_2/gcgdata/geneseq/g: 19: /cgn2_2/gcgdata/geneseq/g: 20: /cgn2_2/gcgdata/geneseq/g: 21: /cgn2_2/gcgdata/geneseq/g: 21: /cgn2_2/gcgdata/geneseq/g: 21: /cgn2_2/gcgdata/geneseq/g: 21: /cgn2_2/gcgdata/geneseq/greaterthan or equal to the scort	Ny analysis of the total SUMMARIES Length DB ID 7 19 V58898 10 20 V59938	10 21 280950 10 21 280950 10 21 284297 11 20 X77658 14 14 040666 14 15 Q78406 14 19 V97198 14 19 V8830 14 19 V8832
Copy OM nucleic - nucleic so Run on: March	Title: US-09-: Perfect score: 7 Sequence: 1 tgttc Scoring table: IDENTI Gapop :	mber of DB seq 1 DB seq 1 cessing:	Database : N_Ger 1: /6 2: /6 3: /6 5: /6 6: /6 6: /6 11: /1 11: /1 12: /1 13: /1 14: /1 15: /1 16: /1 18: /1 18: /1 18: /1 19: /1 19	and its	c 10 7 100.0 c 10 10 10 10 10 10 10 10 10 10 10 10 10

Human dendritic cell SAGE tag, SEQ ID NO:679.

(first entry)

10-APR-2000

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Z78251 standard; DNA; 10

RESULT Z78251

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              This sequence represents a Leptospira DNA sequence isolated from the pathogonic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainei. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a fragment of an intron from the gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkinson's disease related gene; parkin gene; variant; gene therapy;
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                                                                                                                    diagnosis of past or present LS infection.
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Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer \cdot
                                                           SAGE tag: serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL;
                                                                                            cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences 277573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 84; 130pp; English.
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98US-0089993.
98US-0089994.
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98US-0090045.
98US-0090047.
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98US-0090072.
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98US-0089853.
98US-0089878.
98US-00899991.
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98US-0089999.
98US-00900000.
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98US-0090039.
98US-0090040.
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98US-0090042.
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98US-0090079
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                                                                                                              Homo sapiens
                                                                                                                                 WO9965924-A2
                                                                                                                                                                         18-JUN-1999;
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Gaps

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100.0%; Score 7; DB 20; Length 10; 100.0%; Pred, No. 1.4e+04; ive 0; Mismatches 0; Indels

Best Local Similarity 100.0%; Matches 7; Conservative (

Query Match

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with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cell chart transcripts correspond to novel genes. Antigen-presenting cell cativation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MMC (major histocompatibility complex) and subsequent recognition by 7-cell receptors is alone insufficient activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic 7-1ymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly gainst a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in CC an APC; and as hybridisation probes/amplilication primers for the capnormal corresponses belonging to the monocyte lineage. Cells containing these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to abnormal corresponding to the monocyte lineage. Cells containing these genes are used in active immunotherapy (or to stimulate production of a copulation of antigen-specific effector cells) and become antigen specific effectors ensures adequate antigen sond APC-associated costimulatory factors ensures adequate antigens and Presentation of co-stimulatory signals, migration to rodegenous APCs and upregulates the APCs for the correction of I cell growth factors and secretion of chemokines for recruitment of immune effector cells.
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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 7; Conservative 0; Mismatches 0;
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that are preferentially transcribed in the metastatic breast tumour calls.

that are preferentially transcribed in the metastatic breast tumour calls.

to 286677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour calls.

these transcribes can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antispen-encoding sequence for use in gene or call-based vaccines; for diagnosing breast cancer and for raising specific continuously an antispense ancoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antispense used for adoptive for immunothers.
                                                                                                                                                                                     280767 to 283941 represent tags corresponding to distinct transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                      Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer -
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100.0%; Pred. No. 1.4e+04;
iive 0; Mismatches 0;
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                                                                                                                                                  Claim 1; Page 63; 219pp; English.
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98US-0090039
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98US-0090041
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 Shankara S;
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Best Local Similarity
7; Conserve
                                   WPI; 2000-106079/09.
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Roberts BL,
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                                                                                                                                                        that are preferentially transcribed in the metastatic breast tumour colls. 283941 represent tags corresponding to distinct transcribts that are preferentially transcribed in metastatic breast tumour colls. 283942 to 286677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcribts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic biagnosis is by standard immunosasys or hybridisation/amplification reactions. Compounds that modulate expression of the transcribts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based cancernes polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic genes; cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter colls.
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                                                                                  Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer -
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                                                                                                                                         Claim 1; Page 110; 219pp; English
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98US-0090040.
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Best Local Similarity 100.
Matches 7; Conservative
                                       Shankara S;
   (ROBE/) ROBERTS B L. (SHAN/) SHANKARA S.
                                                              WPI; 2000-106079/09.
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19-JUN-1998;
                                        Roberts BL,
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that are preferentially transcribed in the metastatic breast tumnour cells.

that are preferentially transcribed in the metastatic breast tumnour cells.

that are preferentially transcribed in metastatic breast tumnour cells). 283942

to 286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumnour cells).

trissue (i.e. are downregulated in metastatic breast tumnour cells).

These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, or e.g. therapeutic genes (also ribozymes or antisense sequences).

Compounds that an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for adoptive
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Pred. No. 1.4e+04;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                            prevention and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 153; 219pp; English.
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100.0%;
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ID X77658 standard; DNA; 11 BP.
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                                                                                                                                      Roberts BL, Shankara
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Best Local Similarity
7; Conserva
(GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
                                                                                                                                                                                                      WPI; 2000-106079/09
                                                                      SHAN/) SHANKARA S.
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21-NOV-1997;
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                                                                                                                                                                 This invention describes a novel method allowing essential or functional genes to be rapidly identified and inactivated. The method is able to firstly identify most of the essential genes in an organism (1.e. a bacteria or a eukaryote) needed for survival, and secondly it provides for reducing or inactivating their expression. The method is able to lagnostic reagents and therapeutics. The method provides a means for identify functional oligonucleotide molecules able to be used as diagnostic reagents and therapeutics. The method provides a means for identifying essential genes whose sequence is known only as part of a genome with unknown function, as well as a means for identifying conciler acid molecule comprising (a) a first reporter gene encoding a nucleic acid molecule comprising a protein of interest (itself translated from an RNA of interest) and a reporter protein, a second reporter gene encoding a concoling a second reporter protein, and (c) a targeting gene encoding a concoling a concoling molecule such as an external guide sequence (EGS), a ribozyme or an antisense RNA and targeted to the RNA of interest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HVR; human; animal; forensic science; paternity testing; diagnosis; animal breeding; hereditary diseases; tumours; allele; loss; chromosomal regions; tumour region identification; ss.
                                                                                                 Identifying and inhibiting functional nucleic acid molecules in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypervariable region detection probe 14C12.
                                          Robertson HD;
                                                                                                                                            Example 3; Page 28; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 100.0%;
Similarity 100.0%;
7; Conservative 0;
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Q40606/c
ID Q40606 standard; DNA; 14 BP.
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            (INNO-) INNOVIR LAB INC
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                                         Nilsen TW,
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                                                                    WPI; 1999-357853/30
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Best Local Similarity
Matches 7; Conserv
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                                         Kindt TJ,
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Gaps
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                                                                                                                       The sequence is that of a polynucleotide probe which may be used in the detection of new hypervariable regions (HVR) in a DNA sequence. HVR represent a fingerprint useful in e.g. forensic science, paternity testing, animal breeding, etc. The probe may be used as part of a method for the efficient detection in humans or other animals, without the use of mini-satellites or primary enrichment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour; anglogenesis; breast tumour; neurofibroma; glloma; glloblastoma; carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut; immunosuppression; oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor beta; TGF-beta; antisense; treatment;
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hereditary illnesses and tumours - by hybridising labelled polynucleotides and analysing genomic DNA of individuals which react with restriction fragments
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                                                                                                                                                                                                                                                                                                                                           100.0%; Score 7; DB 14; Length 14; 100.0%; Pred. No. 1.4e+04; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                              Sequence 14 BP; 4 A; 4 C; 2 G; 4 T; 0 other;
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                                                                                 Example; Page 13; 46pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q78406 standard; DNA; 14 BP
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93EP-0107849
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Best Local Similarity 100.

Matches 7; Conservative
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Schlingensiepen R;
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13-MAY-1993;
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The present invention describes enzymatic nucleic acid molecules with RNA-cleaving activity (e.g. ribozymes) which are capable of modulating the expression of plant genes: (i) involved in biosynthesize or (ii) involved in flower formation. V9598 to V9634, and alrabids: or (ii) involved in flower formation. V9598 to V96334, and V96335 to V96335 to V96334 represent potato solanidine glucosyltransferase v96335 to V96334 represent potato solanidine glucosyltransferase target V96355 to V96734 represent potato solanidine glucosyltransferase target sequences. V96734 to V9710, and V97171 to V97195 represent potato citrate synthase hammerhead and hairpin ribozymes, respectively. V96735 citrate synthase hammerhead and hairpin ribozymes, respectively. V96735 citrate synthase hammerhead and hairpin ribozymes of the present potato citrate synthase target to V96772, and V97196 to V97220 represent potato citrate synthase target sequences. Ribozymes of the present invention can be used to inhibit spectob but also tomato, pepper, aubergine and ditura or to inhibit for potato but also tomato, lettuce, spinach, cabbage, brussel sprouts, flowering in potato, lettuce, spinach, cabbage, brussel sprouts, flowering in potato, lettuce, spinach, turnip, sweet potato and turf arso the ribozymes can be used for RNA manipulation in the same way that restriction endonucleases are for RNA manipulation in the same companied of the present of the present of the commine way that restriction endonucleases are for DNA, as well as to examine
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See 078352-078488. The sequences given in GENESEQ files 078352-078407 and 078488 are antisense oligodeoxynucleotides of TGF-beta 1. The sequences given in GENESEQ files 078408-78487 are antisense oligodeoxynucleotides of TGF-beta 2 in the form of
                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Solanidine; glucosyltransferase; potato; citrate synthase; ta
hammerhead ribozyme; hairpin ribozyme; alkaloid biosynthesis;
flower formation; cleavage; solanaceous plant; ss.
                                                                                                                                                                                   100.0%; Score 7; DB 15; Length 14; 100.0%; Pred. No. 1.4e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potato citrate synthase target sequence position 123.
                                                                                                                            Sequence 14 BP; 3 A; 3 C; 4 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0979416.
97US-0036545.
97US-0036599.
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V97198/c
ID V97198 standard; RNA; 14 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1999 (first entry)
                                                                                          phosphorothicate analogues
                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                1 tgttgga 7
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                                                                                                                                                                                                                                                                                                           WO9832843-A2
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28-JAN-1997;
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V48709-886 represent antisense oligonucleotides directed against the CETAB-2 gene. Of these, only oligonucleotides V48709-91 resulted in significant redcution in ErbB-2 protein expression, while considered value of the significant redcution in ErbB-2 protein expression, while colliquoucleotides V48792-886 had little effect. The oligonucleotides v48792-886 had little effect. The oligonucleotides colliquoucleotides v48792-886 had little effect. The oligonucleotides consecution. The specification describes oligonucleotides that contain three hydrogen bonds to cytosine; do not contain four consecutive exptosines; do not contain two sequences of three consecutive consecutive cytosines; do not contain two sequences of three consecutive cytosines, and the ratio between residues able to form two H-bonds each cytosines, and the ratio between residues able to form two H-bonds each cytosines, and the ratio between residues able to form two H-bonds each colliquous clottides are used to modulate expression of genes, particularly colliferation of primary cell cultures (e.g. bone marrow stem, liver or proliferation of primary cell cultures (e.g. bone marrow stem, liver or proliferation cells, osteochasts, osteochasts, osteoblasts and/or keratinocytes). The colligonucleotides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases considered the consecution of proteins of consecution of cancer or (targeting TGF) for stimulating the immune system.
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ribozymes can be targeted to specific genes or to consensus sequences within a family of related genes, and being catalytic need to be present at only very low concentrations.
                                                                                                                                                                                       Gaps
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                                                                                                                                              Length 14;
                                                                                                                                                                                       Indels
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                                                                                                                                                           Mismatches 0.
                                                                                                                                           100.0%; Score 7; DB 19;
ilarity 100.0%; Pred. No. 1.4e+04
Conservative 0; Mismatches 0
                                                                                   Sequence 14 BP; 4 A; 4 C; 5 G; 1 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity
Matches 7; Conserv
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13 TGTTGGA 7
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V48830/c
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Pred. No. 1.4e+04;

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The state of these, only oligonal colleges used and state of these, only oligonal colleges used and state of these, only oligonal colleges with the state of these, only oligonal colleges with the invention. The specification describes oligonal colleges can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four consecutive nucleotides able to form three H-bonds each to four consecutive cutosines; do not contain two sequences of three consecutive cutosines; and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The cytosines, and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The cytosines are used to modulate expression of genes, particularly the genes for p53, EEB-2, junb, junb, 7GF-beta 1 or beta 2 to control proliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoblasts and/or keratinocytes). The coligonacleotides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting TGF) for stimulating the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparation of antisense oligo:nucleotide(s) which lack long runs of consecutive quancisine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V48709-886 represent antisense oligonucleotides directed against the
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                                                        Length 14;
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                                                        DB 19; L
1.4e+04;
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Sequence 14 BP; 5 A; 4 C; 0 G; 5 T; 0 other;
                                                                                         Mismatches
                                                      Score 7;
Pred. No.
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100.0%;
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                                                      Query Match 100.

Best Local Similarity 100.

Matches 7; Conservative
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Homo sapiens.
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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl Nydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. A16735 to 6 A17167 and A17622 represent ribozyme sequences for ANT and A17621 to A17682 to A18785 and A1987 to A197814 represent their corresponding target sequences; A19723 to A19222 represent their corresponding target sequences; A19735 to A19222 represent their corresponding target sequences; A18786 to A21861 and A21895 to A22475 and A22363 to A23342 represent their corresponding target sequences; A18785 to A21895 to A21895 to A22475 and A22363 to A23363 to A23362 to A23363 to A23365 to A23425 represent their corresponding target sequences; A23262, A23343 to A23262 to A21895 to A22475 and A22363 to A23362 to A23362 to A23422 represent their corresponding target sequences. The ribozymes sequence for integrin subunit beta 3, and A22476 to A32362, A23343 to A23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding anglogenic factor. Tie-2. They are especially used to treat cancer, diabetic retinopathy, as meovascular degeneration (RNMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, soriasis, verruca vulgaris, angiofibrome of tuberous sclerosis, pot vulgaris, angiofibrome of tuberous sclerosis, other wheber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; anglogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; anglogenic factor; cytostatic; antidabetic; ophthalmologic; antidiflammatory; antiarthitic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; veruca vulgaris; anglofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an anglogenic factors
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                                            Indels
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                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jarvis T,
100.08; Pr. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0079678.
                                                                                                                                                                                                                                                   A21661 standard; RNA; 14 BP
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                                                                                                                                                                                                                                                                                                                                              19-JUN-2000 (first entry)
                 Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-591315/50.
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                                                                                                                                                    ö
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme; target; substrate; catalyst; modulation; expression; Raf gene; delivery; screening; identification; synthesis; deprotection; purification; cancer; inflammation; psoriasis; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphospheres used as antiviral agents and synthons
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A, Kisich K, Matulic-Adamic J, McSwiggen JA;
Reynolds M, Sweedler D, Thompson J, Workman CT;
                                                                                                 Length 14;
                                                                                                         Score ', ___ Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human C-raf target sequence nucleotide position 1952.
                                                                                                   100.0%; Score 7; DB 20;
                           other;
                                                                                                                                                       3; Mismatches
                        5 A; 1 C; 4 G; 4 U; 0
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97US-0049002.
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ID V92044 standard; RNA; 14 BP.
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09-JUN-1997;
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                             Sequence 14
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mutations in diseased cells and to determine c-raf RNA. Specifically NACS with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. V90922 to V93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes the detection of drug-selected mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of drug-selected mutations in the HIV protease gene used to treat HIV infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wild type and mutated protease sequences. The method allows rapid and reliable detection of drug-selected mutation in HIV.
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                                                                                                                                                                                                                                  Length 14;
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1.4e+04;
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                                                                                                                                                                       Sequence 14 BP; 4 A; 5 C; 3 G; 2 U; 0 other;
                                                                                                                                                                                                                                    Score 7; DB 2
Pred. No. 1.46
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV-1 protease gene probe SEQ ID NO:275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 40; 76pp; English.
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100.0%;
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Best Local Similarity 100.
Matches 7; Conservative
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0; Gaps
Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 7; Conservative 0; Mismatches 0; Indels
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Search completed: March 27, 2001, 08:22:59 Job time: 5301 sec

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AF003953 LIU94974 LIU94975 LIU94976 LIU94977 AEU094978 AB007012 ARTHRNS2X AF18737379 AF137379

U60594 Leptospira AB007014 Spirochae AF003953 Leptospir

Description

SUMMARIES

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DB

AC015209 Drosophil AC007475 Drosophil AE003823 Drosophil L48441 Echinochloa AL109850 S.pombe c

AC015209 AC007475 AE003823 EHBPC44NCP SPCC830

58 30 33 33

AF220067

Drosophil Drosophil

13-0CT-1997

us-09-380-826a-7.rge

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AF003953 283 bp DNA BCT 30-MAY-1998
Leptospira interrogans strain 48/95 16S ribosomal RNA gene, partial
                                                                                                                                                                                                         Spirochaeta Sp.
Bacteria: Spirochaetales; Spirochaetaceae: Spirochaeta.
Bacteria: Spirochaetales; Spirochaetaceae: Spirochaeta.

(bases 1 to 354)

Shin, Masson
Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun Submitted (No-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun Submitted 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria: Spirochatales; Leptospiraceae; Leptospira.
1 (bases 1 to 283)
Woo,T.H.S., Patel,B.K.C., Cinco,M., Smythe,L.D., Symonds,M.,
Norris,M. and Dohnt,M.
Identification of Leptonema by real-time homogeneous assay of uppublished
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2 (pases 1 to 283)

Woo,T.H.S., Patel,B.R.C., Cinco,M., Smythe,L.D., Symonds,M.,
Woo,T.H.S., Patel,B.R.C., Cinco,M., Smythe,L.D., Symonds,M.,
Norris,M. and Dohnt,M.

Direct Submission
Submitted (14-MAY-1997) School of Science, Griffith Universi
Submitted (14-MAY-111, Australia
Brisbane, QLD 4111, Australia
1 . 283

/ Organism="Leptospira interrogans"
/ Strain="Heptospira interrogans"
/ Strain="#48/95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shin, W. Yoshinaga, I., Uchida, A. and Ishida, Y.
Shin, M., Yoshinaga, I., Uchida, A. and Ishida, Y.
Shin, M., Yoshinaga, I., Uchida, A. and Ishida, Y.
Shin, M., Yoshinaga, I., Uchida, A. and Ishidae of Obligate
Phylogenetic analysis by 16S rRNA gene sequencing of Obligate
Phylogenetic analysis by 16S rRNA gene sequencing of Obligate
Oligorizahis isolated from the northern basin of Lake Biwa
(Mesotrophic Lake)
Unpublished (1997)
Unpublished (1997)
In 354

Location/Qualifiers

| Cognisma="Spirochaeta sp."
                                                                                                                                          Spirochaeta sp. (sub_species:Freshwater obligate oligotroph, strain:FO-95) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sub_species="Freshwater obligate oligotroph"
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AB007014 354 bp DNA BCT
Spirochaeta sp. 168 rRNA gene, partial sequence.
AB007014
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Best Local Similarity 95.5%; Pred. No. 25;
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Perolat, P.
Direct Submission
Submitted (12-UUN-1996) Microbiology, Monash University, Wellington Submitted (12-UUN-1996) Australia
Rd., Clayton, VIC 3168, Australia
Location/Qualifiers
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ACO23155 Home sapt
AF775672 Unculture
AF018567 Unidentif
D49367 Lithospermu
Z73136 S.cerevisia
U40812 Strongyloce
U41016 Caenorhabdi
U41545 Caenorhabdi
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ACO5742 Homo sapi
ACO63114 Arabidops
ABO08265 Arabidops
ACO68144 Homo sapi
ACO21015 Homo sapi
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AL078470 Arabidops
Z98052 Human DNA
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(pases 1 to 1481)
Perolat, P., Chappel, R.J., Adler, B., Baranton, G., Bulach, D.M., Billinghuszt, M.L., Letocart, M., Merien, F. and Serrano, M.S. Leptospira fainel sp. nov., isolated from pigs in Australia int. J. Syst. Bacteriol. 48 Pt. 3, 851-858 (1998)
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Leptospira fainei 16S ribosomal RNA gene, partial sequence.
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Adler, B., Chappel, R.J., Baranton, G., Bulach, D.M.,
Billinghurst, M.L., Letocart, M., Merien, F., Serrano, M.S. and
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/strain="Hurstbridge"
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(Cobase)

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1 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
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Bacteria: Spirochaetales; Leptospiraceae; Leptospira.

(bases 1 to 288)

Woo,T.H.S. Swythe,L.D., Symonds,M., Norris,M., Dohnt,M.,

Brenner,D.J. and Patel,B.K.C.

Identification of Leptospira inadai by continuously monitoring

Unpublished
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Leptospira inadai 16S ribosomal RNA gene, partial sequence.
U94975
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Leptospira inadai 16S ribosomal RNA gene, partial sequence.
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Pred. No. 1.4e+02;
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Pred. No. 1.4e+02;
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62 t
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61 c 88 g 6
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60 c 88 g
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Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
1 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
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Leptospira inadai 165 ribosomal RNA gene, partial sequence.
U94976
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Leptospira inadai 165 ribosomal RNA gene, partial sequence.
U94977
2 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brencer,D.J. and Petel,B.K.C.
Direct Submission Patel,B.K.C.
Submitted (24-MRX-1997) School of Science, Griffith Unive
Brisbane, QLD 4111, Australia
Location/Qualifiers
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WOO,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct Submission
Submitted (24-MAR-1997) School of Science, Griffith Unive
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Pred. No. 1.4e+02;
0; Mismatches 2;
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Pred. No. 1.4e+02;
0; Mismatches 2;
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61 c 88 g 62 t
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<1. .>288
/product="16S ribosomal
                                                                                                                                            /organism="Leptospira
/strain="68/94"
/db_xref="taxon:29506"
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/organism="Leptospira
/strain="346/95"
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Best Local Similarity 90.9%;
Matches 20; Conservative ,
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Direct Submission Submission Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Mi-Sun Submitted (05-SEP-1997) to the DDBJ/EMBL/GenBank databases. Safath, Laboratory of Marine Molecular Microbiology, Faculty of Agiculture, Kyoto University; Oiwakecho, Kitashirakawa, Sakyoku, Kyoto, Kyoto 306-01, Japan (E-mail:misun@kais.kyoto-u.ac.jp, Tel:075-753-6224, Fax:075-753-6226)
                                                                                                                                                                                                                                                                                                                                                                              Chases I to 288)
Woo,T. H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct Submission
Submitted (24-MR-1997) School of Science, Griffith University,
Brisbane, QLD 4111, Australia
Location/Qualifiers
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Phylogenetic analysis by 16S rRNA gene sequencing of Obligate
Oligotrophs isolated from the northern basin of Lake Biwa
(Mesotrophic Lake)
                                                                                                                                                                                                                                            Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
1 (bases 1 to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
                                                                                                     LIU94979 288 bp DNA BCT 01-JAN-1998
Leptospira inadai 16s ribosomal RNA gene, partial sequence.
U994979
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Spirochaeta sp. (sub_species:Freshwater obligate oligotroph,
strain:SO-104) DNA.
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Bacteria; Spirochaetales; Spirochaetaceae; Spirochaeta.
1 (bases 1 to 353)
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Spirochaeta sp. 16S rRNA gene, partial sequence.
AB007012
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Pred. No. 1.4e+02;
); Mismatches 2;
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61 c 88 g 6
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<1.,>288
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/strain="1078 VRI"
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                 141 TATTGGATCACAGGATTTGATA 162
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tgttggatcacaagatttgata 22
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Shin,M., Yo
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Bacteria; Splirochaetales; Leptospiraceae; Leptospira.
Bacteria; Splirochaetales; Leptospiraceae; Leptospira.
Woo,T.H.S., Smythe.L.D., Symonds,M., Norris,M., Dohnt,M.,
Bronner,D.J. and Patell,B.K.C.
Bronner,D.J. and Patell,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
                                                                                                                                                                                              'bases I to 288)
Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Direct Submission
Submitted (24-MR-1997) School of Science, Griffith University,
Brisbane, QLD 4111, Australia
Location/Qualifiers
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Leptcspira inadai 165 ribosomal RNA gene, partial sequence.
U94978
U94978.1 GI:2735450
                                                           Bacteria: Spirochaetales; Leptospiraceae; Leptospira.

(bases 1 to 288)

Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,

Brenner,D.J. and Patel,B.K.C.
Identification of Leptospira inadai by continuously monitoring
fluorescence during rapid cycle PCR
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Woo,T.H.S., Smythe,L.D., Symonds,M., Norris,M., Dohnt,M.,
Brenner,D.J. and Patel,B.K.C.
Blrect Solutission
Submitted (24, MAR.1997) School of Science, Griffith Univer
Brisbane, QLD 4111, Australia
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Pred. No. 1.4e+02;

0; Mismatches 2; Indels
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Pred. No. 1.4e+02;
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/organism="Leptospira inadai"
/strain="218/95"
/db_xref="taxon:29506"
                                                                                                                                                                                                                                                                                                                                        /organism="Leptospira inadai"
/strain="268/95"
/db_xref="taxon:29506"
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90.9%;
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Length 288; Indels

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Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

[ (bases 1 to 72590)
Arabidopsis thaliana chromosome II section 214 of 255 of the complete sequence. Sequence from clones T517.
ACC03000 AE002093
ACC03000.2 GI:6598383
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Location/Qualifiers
1.72590
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
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I (bases 1 to 1012)

Taylor,C.B., Bariola,P.A., delCardayre,S.B., Raines,R.T. and
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'LEKWYWPSLSGGSPSSGNGGKGSFWGHEWEKHGTCSSPVFHDEYNYFLTLNLYLKHNY
TDVLYQAGYVASNSEKYPLGGIVTALQNAFHITPEVVCKRDAIDEIRICFYKDFKPRD
CVGSODLTSRKSCKYSLPEYTPLGEAMVLKMPTEREAL"

197 c 217 9 311 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Green, P.J.
RNS2: a senescence-associated RNase of Arabidopsis that diverged
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Arabidopsis thaliana ribonuclease (RNS2) mRNA, complete cds.
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Proc. Natl. Acad. Sci. U.S.A. 90 (11), 5118-5122 (1993)
93281708
                                                  /strain="SO-104"
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    .1012
        "Organism="Arabidopsis thaliana" /db_xref="taxon:3702"
16. .795

    .353
    /organism="Spirochaeta sp."

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Arabidopsis thaliana
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/db_xref="GI:289210"
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Location/Qualifiers
                                                                                                                        /product~"16S rRNA"
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes without significant peptide similarity but with EST similarity to other proteins are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are predicted by tRNAscan-SE (Sean Eddy, CRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/RRNAscan-SE). Simple repeats were identified by repeatmasker (Arian Smit, http://en.edu.edu/eddy/RRNAscan-SE).
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Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D., Fujil, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Feldblyum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M., Koo, H., Moffat, K.S., Cronin, L.A., Shen, M., VanAken, S.E., Umayam, L., Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:2642152. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
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                                                                                                                                                                                                                                                                                                                                                                                                    Venter, J.C.
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.
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mRNA gene

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KGKMCLLFINDLDAGAGEMGGTTQTYUNNQMYNATLANTADNFTNYOLPGMYNKEERA
RVPIICTGNDESTLYAPLIRDGRMEKFYWAPTREDRIGVGKGIFFTDKIKDEDIVTLV
DOFPGGSIDFFGALRARNYDDEVRKFVESLGVEKIGKRLYNSREGPPVFEOPEMTYEK
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COMPLEMENT (17561 . 17639)
/rpt_family="(TA)n"
/otn(-418783 . 18921,19188 . 19352,19496 . 19674,19766 . 19861,
/gene="At2g39740"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="At2g39740"
/note="T517.4; predicted by genscan"
join(18783. 18921,19188. 19352,19496. 19674,19766. 19861,
19965. 20034,20131. 20261,20593. 21237)
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LRGATVQPFGSFVSNLFTRWGDLDISVDLFSGSSILFTGKKQKOTLLGHLLRALRASG
LWYKLQFVIHARVPILKVVSGHQRISCDISIDNLDGLLKSRFLFWISBIDGRRRDLVL
LVKEWAKAHNINDSKTGTFNSYSLSLLVIFHFQTCVPAILPPERVIYPKSAVDDLTGY
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RRNI.DRIAQVEQITSRRLVSECNRNSIIGILTGQHIQESLYRTISLPSQHHANGMHNV
RNLHQQARPQNQQMWSQSYNTPNPPHWPPLJQSRPQQNWTQNNPRNLQGQPPVQG
QTWPVITQTQTQQKSPYKSGNRPLKNTSAGSSQNQGHIGKPSGHMNGVNSARPAYTNG
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                                                             KGKMCCLFINDLDAGAGRMGGTTQTTVNNOWNATLMNIADNPTNVLPGATNARRANT RRANTAR RVPITCTGNDFSTLYAPLINGGTTQTTVNNOWNATLMNIADNPTNVLDEGWYKEENA RVPITCTGNDFSTLAPLINGGTTQTTVNNOWNATLMNIADNPTNVLDEGWYKEENA DGFPGGSIDFFGALRARVYDDEVRKFVESLGVEKIGKRLWNSREGPPVFEGPENTYEK LMEYGNMLVMEGENYKRVQLAETYLSQAALGDANADAIGRGTFYGKGAQQVNLPVPEG CTDPVAENPEPTARSDGTCVYNF" 12599,13713 . 14005,14087 . 14559,14651 . 14736,14836 . 14941,15033 . 15349,15834 . 15878))
                                                                                                                                                                                                                                                    AQSNKKSNGSFKVLAVKEDKQTDGDEWRGLAYDTSDDQQDITRGKGMVDSVFQAPMGT
GTHHAVLSSYEXVSQGLRQYNLDNMMDGFYIAPAFMDKLVVHITKNFLTLPNIKVPLI
LGIWGGKGQGKSFQCELVMAKMGINPIMMSAGELESGNAGEPAKLIRORYREAADLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF165146 109723 bp DNA HTG 01-JUN-2000 Homo sapiens chromosome 8 map 8q12-8q13 clone CTA-397H3, WORKING DRAFT SEQUENCE, 3 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.5%; Score 18.8; E
90.9%; Pred. No. 85;
tive 0; Mismatches
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AF165146.2 GI:8151945
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Best Local Sim:
Matches 20;
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KEYWORDS
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Complement (<10039. 11304)
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lntnrnlrscehppasksatballeldptheledggshcavckenpvlkssaremp
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IWRLPGGGFAYGRIPGGWRGGDRMMPVYYTEVDGGRLGDERLPRRYAWGSRRGGRDGG
GSRERGGGFAGRIMRLFGCFSGSSGSIAAAAAASSGSGSRIRYTRRTRSFSMFSTASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(11453. .11512)
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mRNA gene

CDS

mRNA

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             The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: insights into the architecture of ancestral
                                                                                                                                   Turmel, M., Otis, C. and Lemleux, C.
Direct Submission
Submitted (24 MAR-1999) Biochimie, Universite Laval, Pavillon Charles-Eugene Marchand, Quebec GIK 7P4, Canada
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'translation="MEVNILGLIATALFIlIPTSFLLILYVKTASQQN"
                                                     chloroplast genomes
Proc. Natl. Acad. Sci. U.S.A. 96 (18), 10248-10253 (1999)
99398694
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332. .634
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                                                                                                                                            AUTHORS
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             TITLE
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                                                                                                                                                                             2 (bases 1 to 109723)
Schdy,A., Blechschmidt.K., Schillhabel,M., Baumgart,C., Menzel,U.,
Weber,J., Schattevoy,R. and Rosenthal,A.
Direct Submission
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 109723)
Schudy, A., Blechschmidt, K., Menzel, U., Polley, A., Reichwald, K., Rump, A., Schilhabel, M.B., Taudien, S., Wen, G., Schlegelberger, B., Stabert, R. and Rosenthal, A.
Cibert, R. and Rosenthal, A.
Cincumsome & genence
                                                                                                                                                                                                                                                             Submitted (06-JUL-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany 3 (bases 1 to 109723) Genome Sequencing Center Jena.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-MXY-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On Jun 1, 2000 this sequence version replaced gl:5514637.

* NOTE: This is a "working draft" sequence. It currently consists of 3 contigs. The true order of the pieces is in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 109723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF137379 200799 bp DNA circular PLN 14-SE
Nephroselmis olivacea chloroplast DNA, complete genome.
AF137379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nephroselmis olivacea.
Chloroplast Nephroselmis olivacea
Eukaryota, Viridiplantae; Chlorophyta; Prasinophyceae;
Chlorodendrales; Chlorodendraceae; Nephroselmis.
1 (bases 1 to 200799)
Turmel,M., Otis,C. and Lemieux,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 61961: contig of 61961 bp in length
2 62061: gap of unknown length
2 91746: contig of 29685 bp in length
7 109723: contig of 17877 bp in length.
Location/Qualifiers
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a 22757 c 23188 g 31709 t
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Best Local Similarity 90.9
Matches 20; Conservative
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Chloroplast Nephroselmis olivacea
Chloroplast Nephroselmis olivacea
Chlorodendraies, Chlorophyta; Prasinophyceae;
Chlorodendraceae; Nephroselmis.
1 (bases 1 to 200799)
1 (bases 1 to 200799)
1 Turnel, M., Otis, C. and Lemieux, C.
The complete chloroplast DNA sequence of the green alga
Nephroselmis olivacea: insights into the architecture of ancestral
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proc. Natl. Acad. Sci. U.S.A. 96 (18), 10248-10253 (1999)
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Nephroselmis olivacea chloroplast DNA, complete genome
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Turmel,M., Otis,C. and Lemieux,C.
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                                                                                    complement(8132. .8779)
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Conservative (
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Matches 20; Conserv
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PAKKANHGSTPEPOY ENERNWY KLESLATVGLLFATRLSGLOFNK YTELK SVAEROOIGO

PAKKANHGSTPEPOY ENERNWY KLESLATVGLLFATRLSGLOFNK YTELK SVAEROOIGO

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5489. .6964
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RLDEGDSGICLMHQIDTNTSAQIRRLGVDGIELVHHPQRVYPKRGSFESILGGVDTEG
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QTLISEMIVQEQDPPSYPTVSLFERNM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLEARLY MAY LERRESTS WARRED WATERNELY IGWECVLMIPLLLTA TSVFIIGFIAAPPVDIDGIREPVSGSLLFGNNIISGAIIPSSAAIGIHFYPIWEAASI TSVFIIGFIAAPPVDIDGIREPVSGSLLFGNNIISGAIIPSSAAIGIHFYPIWEAASI DEMLYNGGYELVLHFLLGVAACYMERWELSFRICHRRWIAVASAAYAAATAVLTI YPIGGSFSDGWPLGISGTFRWIIVPOAEHNILMHPFHMLGVAGVFGSLLFFRANGSL VTSSLIRETTENESANAGYKFGGEEETYNIVAAHGYFGRLIFOYASFRNISRSLHFFLA AWPVVCIWFTALGVSTWAFNLNGEVRUNGSVUDSQGRVINTWADIINRANLGMEVWHER
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GAGQEVSVVCEVQQLLGDGLVRAVSMSATDGLMRGMEVTDTGRALSVPVGPTTLGRIF
NVLGEPVDNMOEPVGNEKTLPTHREAPAFVDLOTKLSIFETGIXVVDLLAPYRRGGKIG
LEGGAGVGKTVLIMELINNIAKAHGVVSVFGGGVGETFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SALLGRMPSAVGYQPTLATEMGGLÖERITSTKDGSITSTGAVYVPADDLTDPAPATTF
HDATTVISTSRNLAAKGIYPAVDPLOSTSTWMCONTGORYKGTLORYKEL
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765. .84
Direct Submission
Submitted (24-MAR-1999) Biochimie, Universite Laval, Pavillon
Charles-Eugene Marchand, Quebec GIK 7P4, Canada
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MEVNILGLIATALFIIIPTSFLLILYVKTASQQN"
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1733. .3862
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    TITLE
JOURNAL
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complement(9045..9431)

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IGAPLVELLRGSVSVGQSTLTRFYSLHTFVLPLLTAVFMLMHFLMIRKQGISGPL"
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Best Local Similarity 90.9%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 2; Indels 0;
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Search completed: March 27, 2001, 08:17:15 Job time: 5912 sec

Run on:

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21
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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9b_ssy: *
9b_ssy: *
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9b_ssy: *
em_hun: *
em_nin: *
em_on: *
em_on
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em_htg5:*
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em_htg6:*
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9b_bv: *
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9b_pl1: *
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9b_pr2: *
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gb_ba2:*
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gb_htg8:*
gb_htg9:*
gb_htg10:*
gb_htg11:*
gb_htg11:*
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9b_htg15;
9b_htg16;
9b_htg16;
9b_htg18;
9b_htg19;
9b_htg21;
9b_htg21;
9b_htg21;
gb_pr6:*
gb_pr7:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	120741 Sequence 6	AR082373 Sequence /	I52063 Sequence 5	I78419 Sequence 21	AX007639 Sequence	A88596 Sequence 74	A90563 Sequence 74	AR082368 Sequence	I78414 Sequence 21	AX007638 Sequence	AX007675 Sequence	A35660 Synthetic h	AR045297 Sequence	AR071525 Sequence	I52349 Sequence 90			I61577 Sequence 13	I77301 Sequence 8	I77302 Sequence 9
SUMMARIES	120741	AR082373	152063	178419	AX007639	A88596	A90563	AR082368	178414	AX007638	AX007675	A35660	AR045297	AR071525	I52349	161575	161576	161577	177301	177302
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a Query Match Length DB	11:	13	13	13	14	14	14	14	14	15	15	15	15	15	15	15	15	15	15	15
a Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	7		7	7	7	. 7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
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                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                          Unknown.
Unclassified.
1 (bases 1 to 13)
1 (bases 1, C, Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and Draper, K.G., Thompson, J.D.
HIV nef targeted ribozymes
Patent: US 5972704-A 217 26-OCT-1999;
Location/Qualifiers
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Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                Length 11;
                                                                                               100.0%; Score 7; DB 81; Length 11
100.0%; Pred. No. 6.4e+05;
tive 0; Mismatches 0; Indels
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Unclassified.
1 (bases 1 to 13)
Swiggen,J.A. and Mamone,J.Anthony.
Hammerhead ribozymes for preferred targets
Patent: US 5646020-A 5 08-JUL-1997;
                                                                                                                                                                                                                           PAT
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Sequence 217 from patent US 5972704..
8082373 AR082373.1 GI:10009099
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Sequence 5 from patent US 5646020.
and applications thereof
Patent: US 5516634-A 7 14-MAY-1996;
Location/Qualifiers
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Matches 7; Conservative
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AR082373/c
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152063/c
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Unclassified.
1 (bases 1 to 11)
Newman, P.J. and Santoso, S.S.
Molecular basis of the human platelet bra/brb alloantigen system
                                                                                                                                                                                                                                                                   154826 Sequence 25
                                                                                                                                                                                                                                                                                                                                                                                                                                     Unclassified.
Unclassified.
1 (bases 1 to 11)
Newman, P.J. and Santoso, S.S.
Newman, P.J. and Santoso, S.S.
and applications thereof
patent: US 5516634-A 6 14-MAY-1996;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0;
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Sequence 7 from patent US 5516634.
120742 120742.1 GI:1601097
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Sequence 6 from patent US 5516634.
120741
120741.1 GI:1601096
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AX007650

AX007650

AX007667

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Unclassified.
1 (bases 1 to 14)
Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and
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                                                                                                                                                                                                                                                                          Length 14;
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                                                                                             1 (bases 1 to 14)
Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLEOTIDE PREPARATION METHOD
Patent: WO 9833904-A 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 14)
Brysch,W.D. and Schlingensiepen,K.D.
An antisense oligonucleotide preparation method
Patent: EP 085679-A 05-AUG-1998;
BIOGNOSTIK GES (DE)
Location/Qualifiers
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100.0%; Pred. No. 6.2e+05;
iive 0; Mismatches 0;
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Sequence 744 from Patent EP0856579.
A90563 A90563.1 GI:6739077
Sequence 744 from Patent W09833904.
A88596
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/organism="unidentified"
/db_xref="taxon:32644"
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                             A88596.1 GI:6737166
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Best Local Similarity 100.
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                                                                                                                                                                                                             Draper.K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.
Thompson,J.D.
Patent: US 5693535-A 217 02-DEC-1997;
Location/Qualifiers
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INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aids-associated retrovirus.
Aids-associated retrovirus
Viruses: Retroid viruses; Retroviridae.
1 (bases 1 to 14)
                                                                                                    178419 13 bp DNA
Sequence 217 from patent US 5693535.
178419 17:3014573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Sequence 181 from Patent WO9967428.
AX007639
                                                                                                                                                                                                                                                                                                               /organism="unknown"
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Best Local Similarity 100.

Matches 7; Conservative
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Matches 7; Conserv
            1 tttgata 7
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10 TTTGATA 4
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11 TTTGATA 5
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10 TTTGATA 4
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AX007639/c
LOCUS
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178419/c
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A35660/c
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AX007675/c
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Aids-associated retrovirus
Viruses; Retroid viruses; Retroviridae.
1 (bases 1 to 15)
Stuyver,L.
Method for detection of drug-selected mutations in the hiv protease
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Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.
HIV targeted ribozymes
Patent: US 5691535-A 212 02-DEC-1997;
Location/Qualifiers
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/organism="Aids-associated retrovirus"
/db_xref="taxon:11966"
a 1 c 3 g 6 t
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100.0%; Pred. No. 6.2e+05;
                                                                                                                DB 81; L
. 6.2e+05;
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INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
Location/Qualifiers
Thompson, J.D.
HIV nef targeted ribozymes
Patent: US 5972704-A 212 26-OCT-1999;
Location/Qualifiers
                                                                                                                                                                                                                                         178414 14 bp DNA
Sequence 212 from patent US 5693535.
178414
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                                                                                                               100.0%; Score 7; DB 100.0%; Pred. No. 6.2 Eive 0; Mismatches
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Sequence 180 from Patent W09967428.
AX007638
AX007638.1 GI:9995335
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                                                     /organism="unknown"
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Best Local Similarity 100.0
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synthetic construct
artificial sequence.
1 (bases 1 to 15)
Camble,R. and Edge,M.D.
Analogous interferon polypeptides, process for their preparation and pharmaceutical compositions containing them
Parent: EP 0194006-A 105 10-SEP-1986;
IMPERIAL CHEMICAL INDUSTRIES PLC
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100.0%; Score 7; DB 79; Length 15
nilarity 100.0%; Pred. No. 6.18+05;
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/db_xref="taxon:11966"
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INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
a 4 c 2 g 4 t
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Synthetic human IFN-alpha 2 gene oligo.
A35660
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Viruses; Retroid viruses; Retroviridae.
1 (bases 1 to 15)
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Séquence 217 from Patent W09967428.
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Hz-1 Virus persistence-associated-gene 1 (PAG1) promoter uses therefor, and compositions containing same or products therefrom Patent: US 5911982-A 25 15-JUN-1999;
Location/Qualifiers
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                                                                                                            Unknown.
Unclassified.
1 (bases 1 to 15)
Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb ribozymes having 2'-5'-1inked adenylate residues
Patent: US 5817796-A 90 06-OCT-1998;
                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 7; DB 81; Length 15; Best Local Similarity 100.0%; Pred. No. 6.1e+05; Matches 7; Conservative 0; Mismatches 0; Indels
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                         AR045297 15 bp DNA
Sequence 90 from patent US 5817796.
AR045297
AR045297.1 GI:5966762
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Sequence 25 from patent US 5911982.
AR071525 GI:7222413
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/organism="unknown"
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RESULT 14
AR045297/c
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AA65499 V18 F02.r
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AU010246 AU010246
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AZ458268 IM0262N11
DZ5852 HUMCSGN11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ386406 19 bp DNA GSS 02-OCT-2000
1M0145C22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0145C22 F, DNA sequence.
AZ386406
AZ386406 GI:10500106
                                       pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                          Description
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10 AZ32837

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10 D20685

5 T70764

8 AQ025921

3 HSM007685

3 AZ495773
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TITLE

COMMENT

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10.5 Kb range using preparative agarose gel electrophoresis. Vector DN was prepared from a derivative of pWD42 (gild732114 [gb]AR123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                            1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 7; DB 173; Length 20; 100.0%; Pred. No. 1.5e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0311 row: C column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                University of Utah Genome Center University of Utah
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Location/Qualifiers
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Contact: Robert B.
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

(bases 1 to 19)

Lonn, D., Aoyadi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Emall: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
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                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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FEATURES

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ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through of .05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to adaptored DNA was purified and size-selected for a 9.5 to electrophoresis. Vector DNA was prepared from a derivative of pwns. Property of plasmid R1. The vector was ligated inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance.
                                                                                                                                      Enkaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Entheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. 1 (bases 1 to 21)

S Dun,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Mesen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A. plasmid inserts
Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
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1M0350A24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0350A24 R, DNA sequence.
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/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-OCT-2000
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Insert Length: 10000 Std Error: 0.00
Plate: 0249 row: E column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmld ends
High quality sequence stop: 21.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="UUGC1M0249E13"
AZ450829.1 GI:10606020
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Fax: 801 585 7177
                                                                                                          house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Robert B. Weiss
Contract: y of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0249E13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0249E13 R, DNA sequence.
                                                                                                                                           Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

10 (bases 1 to 21)

11 (bases 1 to 21)

12 (bases 1 to 21)

13 (bases 1 to 21)

14 (bases 1 to 21)

15 (bases 1 to 21)

16 (bases 1 to 21)

17 (bases 1 to 21)

18 (bases 1 to 21)

19 (bases 1 to 21)

19 (bases 1 to 21)

19 (bases 1 to 21)

10 (bases 1 to 21)
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@qenet
                                                            SSS.
house mouse.
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source

FEATURES

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DEFINITION AZ450829/C

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BASE COUNT ORIGIN

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1. .25
//doganisma="Homo sapiens"
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/clone="IMAGE:1667037"
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polylinker V_TYPE: phagemid; Site_1: Not I: Site_2: Eco RI
: 1st strand cDNA was primed with a Not I - oligo(dT)
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 25) NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
  clone IMAGE:1667037 3' similar to TR:064507 Q64507 SERINE 1 ULTRA HIGH SULFUR PROTEIN. ; contains PTR5 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI158948 25 bp mRNA EST 02-OCT-1998 ui42e07.x1 Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:1885092 3' similar to TR:Q90658 Q90658 ZINC FINGER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 2304 Std Error: 0.00
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100.0%; Score 7; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/G0 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymorieotide kinase. Adaptor oligonacleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (q1147321141gb]APL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the linsert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Warsity of Utah
Wan 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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DEFINITION 0927b11.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens CDNA
                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/sex="Male"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0350 row: A column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
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AZ508369.1 GI:10689781
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                 house mouse.
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3 TGTTGGA 9
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Gaps .; ;

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Trace considered overall poor quality
Insert Length: 1074 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

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I. .25
I. .2
Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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1 (bases 1 to 26)
10 (bases 1 to 26)
11 (bases 1 to 26)
12 (bases 1 to 26)
13 (bases 1 to 26)
14 (bases 1 to 26)
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184112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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100.0%; Pred. No. 1.6e+05;
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Insert Length: 10000 Std Error: 0.00
Plate: 0090 row: M column: 13
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                        www-bio.llnl.gov/bbrp/image/image.html
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/organism="Mus musculus"
/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Jases 1 to 25)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information
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                Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. Waterston, R.
The Washlu-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washlu-HHMI Mouse EST Project
Washlu-HMI Mouse Park Parkway, Box 8501, St. Louis, MO 63108
Teat: 314 286 1800
Feax: 314 286 1810
Email: mouseest@watson.wustl.edu
                Soares, B., Wilson, R. and
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Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
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Matches 7; Conservative 0; Mismatches 0;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Contact: Robert B. Weiss
University of Utah Genome Center
Rui 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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1M0061N14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0061N14 F, DNA sequence.
                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                             /clone_lib="Mouse 10kb plasmid UUGClM library"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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ORIGIN
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DEFINITION
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Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Welss
University of Utah Genome Center
University of Utah
RR. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ419519 29 bp. DNA GSS 03-OCT-2000
IM0196N03F Mouse 10kb plasmid UUCCIM library Mus musculus genomic
clone UUGCIM0196N03 F, DNA sequence.
                                                                                                                                                                      /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain xL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 7; DB 170;
100.0%; Pred. No. 1.6e+05;
tive 0; Mismatches 0;
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Class: plasmid, ends
High Acceptage
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Location/Qualifiers
1. 29
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Insert Length: 10000 Std Erro
Plate: 0196 row: N column: 03
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Best Local Similarity 100.

Matches 7; Conservative
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Fax: 801 585 7177
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house mouse.
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AZ357647/C
LOCUS
DEFINITION
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ORIGIN
source
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KEYWORDS
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                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubAl 1919[AP12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dipublished (2000)
Contact: Robert B. Welss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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1M0062B09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0062B09 F, DNA sequence.
                                                                                                                          /sex="Male"
/lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                               /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: B column: 09
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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Location/Qualifiers
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Best Local Similarity 100...
7; Conservative
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KEYWORDS
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/lab host-"E. Coli strain XL10-Gold, Tl-resistant, F-"
/note-"Vector: PWD42nv; Purified genomic DNA from M.
musculus G75BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114)gb]ARL29072.1), a copy-number.
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the linsert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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AL Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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/db_xref="taxon:10090"
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Best Local SImilarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAAGGACGCCAGT
Class: plasmid ends
High quality sequence stop: 31.
/organism="Mus musculus"
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                                                                                                                                                                             /sex="Male"
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Fax: 801 585 7177
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FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|q'32114|qp)laft29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ328463 32 bp DNA GSS 29-SEP-2000
1M0052D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0052D18 F, DNA sequence.
                                                                                                                                                                                                                                                                                                /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                           /clone_lib="Mouse 10kb plasmid UUGCIM library"
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100.0%; Pred. No. 1.6e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: D column: 18
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                                                                                       /organism="Mus musculus"
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High quality sequence stop: 32.
Location/Qualifiers
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Fax: 801 585 7177
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84112, USA
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Duni, D., Aoyal, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ320254 32 bp DNA GSS 29-SEP-2000
1M0040P07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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AZ320254
AZ320254.1 GI:10371848
                                                                                                                                                                                                                                                                    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0\$; Score 7; DB 171; Length 31; Best Local Similarity 100.0\$; Pred. No. 1.6e+05; Matches 7; Conservative 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0040 row: P column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                        /organism="Mus musculus"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                              /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0099D19"
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Fax: 801 585 7177
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KEYWORDS
SOURCE
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ORIGIN

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TITLE

COMMENT

Gaps ; 0

Length 32; Indels

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musculus G57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerses and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gen
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114 gb) RR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance."

    .32
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                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC1M0052D18"
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
                                                                                                                                                                                                             /strain="C57BL/6J"
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0 Gaps ö Query Match 100.04; Score 7; DB 170; Length 32; Best Local Similarity 100.04; Pred. No. 1.6e+05; Matches 7; Conservative 0; Mismatches 0; Indels

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Search completed: March 27, 2001, 07:38:21 Job time: 4584 sec

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em\_esthum10:\*
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em\_esthum16:\*
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em\_estin3: em\_estin4: em\_estov1:

em\_estpl1 em\_estpl2

em\_estpl

em\_estov2

em\_estpl5 em\_estrol

em\_estro2

em\_estin2

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March 27, 2001, 07:38:17 ; Search time 2517.78 Seconds (without alignments) 61.230 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                    7991742 segs, 3503743858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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gb\_est73:\*
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gb\_est7;

gb\_est69

b\_est67 b\_est68

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gb\_est53: gb\_est54 gb\_est55

em\_estrol3:\*

9b\_est41:\*

9b\_est43:\*

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9b\_est46:\*

9b\_est46:\*

9b\_est47:\*

9b\_est49:\*

9b\_est60:\*

9b\_est50:\*

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17.8 80.9 600 138 BF006444 17.8 80.9 633 138 BF006444 17.4 79.1 286 126 BB288727 17.4 79.1 529 128 BAW695022 17.4 79.1 674 94 AW695022 17.4 79.1 674 94 AW695022 17.4 79.1 674 94 AW695022 17.4 79.1 1010 190 CNS00D26 17.2 78.2 151 134 BB068225 17.2 78.2 435 159 AQ595814 17.2 78.2 437 16 AQ2121715 17.2 78.2 500 24 AN733664 17.2 78.2 500 24 AN777095 17.2 78.2 500 24 AN777095 17.2 78.2 500 100 CNS00D30 17.2 78.2 500 24 AN777095 17.2 78.2 500 24 AN7777095 17.2 78.2 500 24 AN7777095 17.2 78.2 500 24 AN7777095 17.2 78.2 500 24 AN7777914 17.3 78.2 500 24 AN7777914 17.4 78.2 500 24 AN7777914 16.8 76.4 250 104 BEL18999 16.8 76.4 446 24 AN7777914 16.8 76.4 446 24 AN7777919 16.8 76.4 446 24 AN777779 16.8 76.4 446 24 AN777779 16.8 76.4 446 24 AN77777779 16.8 76.4 446 24 AN777777777777777777777777777777777777		18	7	83.6	934	191	CNSO2BWA	AL190387 Tetrao
17. 8 10. 9 10. 9 10. 10. 10. 10. 10. 10. 10. 10. 10. 10.		17	<b>&amp;</b>	6.08	600	138	BF006444	BF006444 EST434 BF006254 EST434
17.4 79.1 677 110 BE581720 17.4 79.1 529 158 A0497779 17.4 79.1 529 158 A0497779 17.4 79.1 529 158 A0497779 17.4 79.1 762 106 BE283043 17.4 79.1 101 190 CKSOODZ6 17.2 78.2 425 15 A1049911 17.2 78.2 437 165 A0795184 17.2 78.2 437 165 A0795182 17.2 78.2 437 165 A0795182 17.2 78.2 531 159 A0223715 17.2 78.2 531 150 A0223715 17.2 78.2 531 150 A022347 17.2 78.2 531 150 A023477 17.2 78.2 531 150 A043477 17.2 78.2 546 24 A1777095 17.2 78.2 546 14 B67515 17.2 78.2 546 14 B67515 17.2 78.2 549 192 CKSG4HNP 17.2 78.2 549 192 CKSG4HNP 17.2 78.2 680 174 B57384 17.2 78.2 680 174 B57383 16.8 76.4 260 104 BE118999 16.8 76.4 396 97 AW487391 16.8 76.4 446 24 A1761541 16.8 76.4 446 24 A1761541 16.8 76.4 446 156 A0332265 16.8 76.4 450 138 BF002933 16.8 76.4 450 138 B70383 16.8 76.4 450 138 B703	٠	17	<b>x</b> <	80.9	286	126	BF006234 BB288727	BB288727 BB2887
17.4 79.1 529 158 AQ497779 17.4 79.1 674 94 AW695022 17.4 79.1 674 106 BEE42809 17.4 79.1 1101 190 CNSO0D26 17.2 78.2 425 15 A1049911 17.2 78.2 425 15 A1049911 17.2 78.2 432 150 AQ221715 17.2 78.2 432 150 AQ221715 17.2 78.2 439 162 AQ796989 17.2 78.2 530 24 A1733664 17.2 78.2 536 39 AW034253 17.2 78.2 536 39 AW634253 17.2 78.2 546 24 A1777095 17.2 78.2 549 102 CNSQ4HNP 17.2 78.2 649 191 CNSQ4NNP 17.2 78.2 649 192 CNSQ4HNP 17.2 78.2 649 192 CNSQ4HNP 17.2 78.2 649 192 CNSQ4NNP 17.2 78.2 649 192 CNSQ4NNP 17.2 78.2 649 192 CNSQ4NNP 17.2 78.2 649 194 CNSQ2391 16.8 76.4 260 104 BEI18999 16.8 76.4 260 104 BEI18999 16.8 76.4 446 24 A1761541 16.8 76.4 446 24 A1761541 16.8 76.4 446 24 A1761541 16.8 76.4 446 156 AQ332265 17.8 76.4 446 156 AQ332265 18.8 76.4 446 156 AQ332265 18.8 76.4		17	* 4	79.1	407	110	BE581720	BE581720 kq51c0
17.4 79.1 674 94 AMM95022 17.4 79.1 674 106 BE642809 17.4 79.1 101 190 CNSODD26 17.2 78.2 425 15 AIQ49911 17.2 78.2 431 159 AO22212 17.2 78.2 431 159 AO22212 17.2 78.2 437 146 W42212 17.2 78.2 437 146 W42212 17.2 78.2 500 24 AI73864 17.2 78.2 536 39 AW04223 17.2 78.2 536 39 AW04223 17.2 78.2 536 39 AW04223 17.2 78.2 536 39 AW0523477 17.2 78.2 536 39 AW0523477 17.2 78.2 536 39 AW0523477 17.2 78.2 546 24 AI777095 17.2 78.2 546 24 AI777095 17.2 78.2 649 102 CNSO4HNP 17.2 78.2 698 168 AZ193715 17.2 78.2 699 104 B57784 17.2 78.2 699 104 B57784 17.2 78.2 699 104 B57784 17.2 78.2 699 104 B57784 17.2 78.2 699 104 B5118999 17.2 78.2 699 104 B57784 17.2 78.2 699 104 B57784 17.2 78.2 699 104 B57784 17.2 78.2 699 168 AZ193715 16.8 76.4 260 104 BE118999 16.8 76.4 260 104 BE118999 16.8 76.4 450 138 BF002933 16.8 76.4 450 138 BF002933 16.8 76.4 450 138 BF002933 16.8 76.4 464 156 AO332265 16.8 76.4 464 156 AO332265 16.8 76.4 464 156 AO332265 16.8 76.4 460 138 BF002933 16.8 76.4 460 138 BF002945 17.7 7		17	4	79.1	529	158	AQ497779	AQ497779 HS_506
17.4 79.1 70.2 100 BE6428043 17.4 79.1 101 190 CNSO0D26 17.2 78.2 151 134 BE668225 17.2 78.2 431 159 A0595814 17.2 78.2 431 159 A0595814 17.2 78.2 432 150 A0221715 17.2 78.2 432 150 A0221715 17.2 78.2 439 16.2 A079689 17.2 78.2 524 174 B65282 17.2 78.2 534 150 A042347 17.2 78.2 534 174 B65282 17.2 78.2 536 39 AW044253 17.2 78.2 54 174 B65282 17.2 78.2 560 24 A1779914 17.2 78.2 560 24 A1779914 17.2 78.2 560 197 AW95686 17.2 78.2 560 197 AW95686 17.2 78.2 569 168 A2777995 17.2 78.2 569 168 A2777995 17.2 78.2 599 191 CNSC29DN 17.2 78.2 569 168 A2777995 17.2 78.2 569 168 A7777995 17.2 78.2 569 174 B57382 16.8 76.4 296 175 AW943311 16.8 76.4 396 97 AW443311 16.8 76.4 446 24 A1761541 16.8 76.4 446 24 A1761541 16.8 76.4 446 24 A1761541 16.8 76.4 446 156 A0332265 16.8 76.4 446 156 A0332233 16.8 76.4 446 156 A0332233	-	17	4	79.1	674	46	AW695022	AW6930022 NF 06250
17.4 79.1 10.1 150 CNSODES 11.2 78.2 115.1 134 BE068225 11.2 78.2 13.1 159 AOS95814 11.2 78.2 43.1 159 AOS95814 11.2 78.2 43.1 159 AOS95814 11.2 78.2 43.1 159 AOS95814 11.2 78.2 43.9 162 AO796989 11.2 78.2 43.9 162 AO796989 11.2 78.2 50.0 24 AN733664 11.2 78.2 50.0 24 AN779714 11.2 78.2 50.0 24 AN779714 11.2 78.2 50.0 24 AN779714 11.2 78.2 50.0 14 BE11899 11.2 78.2 61.9 97 AW963686 11.2 78.2 61.9 97 AW96399 11.2 78.2 61.9 97 AW96399 11.2 78.2 61.4 19.1 CNSO29DN 17.2 78.2 61.2 78.2 78.2 78.2 78.2 78.2 78.2 78.2 78	14	17	4.	79.1	762	1100	BE283043	BE642809 Cri2_7
17.2   78.2   151   134   BE068225   17.2   78.2   425   15   A1049911   17.2   78.2   425   15   A1049911   17.2   78.2   432   159   A0221715   17.2   78.2   439   162   A0721715   17.2   78.2   439   162   A0721712   17.2   78.2   439   162   A073164   17.2   78.2   531   150   A0223477   17.2   78.2   534   174   B65282   17.2   78.2   534   174   B65282   17.2   78.2   546   24   A1779714   17.2   78.2   546   24   A1779714   17.2   78.2   619   97   AM034253   17.2   78.2   619   97   AM034266   17.2   78.2   619   97   AM03866   17.2   78.2   619   97   AM03866   17.2   78.2   619   97   AM03866   17.2   78.2   649   191   CNSO29DN   17.2   78.2   649   191   CNSO29DN   17.2   78.2   649   192   CNSO4HNP   17.2   78.2   649   194   CNSO29DN   17.3   37.3   37.4   47.3   37.3   47.4   47.3   47.4		17	4.4	79.1	1101	190	CNS00DZ6	AL077427 Drosop
17.2 78.2 425 15 AI049911 17.2 78.2 431 159 AO595814 17.2 78.2 431 150 AO521715 17.2 78.2 437 146 W42212 17.2 78.2 437 146 W42212 17.2 78.2 500 24 AI733664 17.2 78.2 524 174 B62582 17.2 78.2 536 39 AW034253 17.2 78.2 536 39 AW034253 17.2 78.2 546 24 AI77714 17.2 78.2 546 24 AI777095 17.2 78.2 614 105 BE187570 17.2 78.2 614 105 BE187570 17.2 78.2 614 105 BE187570 17.2 78.2 698 168 A219715 17.2 78.2 698 168 A219715 17.2 78.2 698 168 A2193715 16.8 76.4 260 104 BE118999 16.8 76.4 396 97 AW48726 16.8 76.4 446 24 A761541 16.8 76.4 446 24 A761541 16.8 76.4 446 156 A0332265 16.8 76.4 446 156 A0332265 16.8 76.4 461 156 A0332265 16.8 76.4 461 156 A0332265 16.8 76.4 A46 156 A0332265 17.3 A0532040 Arabidopsis thaliana flower buds COI  AV532040 A754040 A168666444444444444444444444444444444444		17	. 7	78.2	151	134	BE068225	BE068225 MR4-BT
17.2 78.2 431 159 A0921814 17.2 78.2 437 159 A0921814 17.2 78.2 437 146 W43212 17.2 78.2 437 146 W43212 17.2 78.2 439 162 A0796989 17.2 78.2 504 174 B65582 17.2 78.2 531 150 A0223477 17.2 78.2 534 174 B65533 17.2 78.2 579 174 B67515 17.2 78.2 579 174 B67515 17.2 78.2 579 174 B67515 17.2 78.2 619 97 AW96886 17.2 78.2 619 197 AW96329N 17.2 78.2 619 197 AW9784 17.2 78.2 619 192 CNSO4HNP 17.3 76.4 296 145 T20362 16.8 76.4 450 138 BF002933 16.8 76.4 464 156 A0332265 16.8 76.4 464 156 A0332233			7	78.2	425	15	AI049911	AIO49911 an30hU
17.2 78.2 437 136 W42317.1 17.2 78.2 437 146 W42312.1 17.2 78.2 439 162 A0796989 17.2 78.2 524 174 B62282 17.2 78.2 534 174 B62282 17.2 78.2 534 150 A0223477 17.2 78.2 536 39 W4034253 17.2 78.2 54 A1779714 17.2 78.2 54 A1779714 17.2 78.2 54 A1779714 17.2 78.2 54 A1779714 17.2 78.2 614 105 BE18750 17.2 78.2 619 17 AW956586 17.2 78.2 619 197 AW956586 17.2 78.2 698 168 A277795 17.2 78.2 698 174 B57789 17.2 78.2 904 191 CNSCQ5DN 17.2 78.2 949 192 CNSQ4HNP 17.2 78.2 948 192 CNSQ4HNP 18.8 76.4 446 24 A1761541 16.8 76.4 446 24 A1761541 16.8 76.4 446 156 A0332265 16.8 76.4 46 156 A0332233			9	78.2	431	159	AQ595814	AQ393614 HS_21:
17.2 78.2 439 162 A0796989 17.2 78.2 500 24 A733664 17.2 78.2 500 24 A733664 17.2 78.2 500 24 A733664 17.2 78.2 511 150 A0223477 17.2 78.2 536 39 AW034253 17.2 78.2 536 39 AW034253 17.2 78.2 579 174 B67515 17.2 78.2 614 105 BE187570 17.2 78.2 619 97 AW963686 17.2 78.2 680 174 B57784 17.2 78.2 680 174 B57784 17.2 78.2 680 174 B57784 17.2 78.2 6904 191 CNS029DN 17.2 78.2 904 191 CNS029DN 18.2 904 191 CNS029DN 18.2 904 192 CNS029DN 18.2 904 193 CNS029DN 18.2 904 192 CNS029DN 18			, c	78.7	432	146	M43212	W43212 22591 Le
17.2   78.2   500   24   AI733664     17.2   78.2   534   174   B65282     17.2   78.2   534   150   A0223477     17.2   78.2   536   39   AW034253     17.2   78.2   536   39   AW034253     17.2   78.2   546   24   AI779714     17.2   78.2   619   97   AW053866     17.2   78.2   619   97   AW053866     17.2   78.2   680   174   B57784     17.2   78.2   680   174   B57784     17.2   78.2   694   168   AZ13375     17.2   78.2   949   192   CNSG4NNP     16.8   76.4   250   104   BEI18999     16.8   76.4   396   97   AW487226     16.8   76.4   446   24   AI761541     16.8   76.4   450   138   BF002933     16.8   76.4   450   138   BF002933     16.8   76.4   464   156   AO332265     AV532040   Arabidopsis thaliana flower buds Col     AN532040   Arabidopsis thaliana flower Sequence     AV532040   AV532040   AV532040     AV532040   AV532040   AV532040     AV532040   AV532040   AV532040     AV532040   AV532040     AV532040   AV532040     AV532040   AV532040     AV532040   AV532040     AV532040   AV532040     AV532040   AV532040     AV532040   AV532040     AV532040   AV532040     AV532040   AV532040     AV532040   AV532040     AV532040   AV532040     AV532040   AV532040     AV			10	78.2	439	162	AQ796989	AQ796989 nbxb00
17.2 78.2 524 174 B62282 17.2 78.2 534 174 B62282 17.2 78.2 536 39 AW034253 17.2 78.2 546 24 A177914 17.2 78.2 546 24 A177914 17.2 78.2 614 105 BE187570 17.2 78.2 614 105 BE187570 17.2 78.2 680 174 B67584 17.2 78.2 698 168 A2193715 17.2 78.2 698 168 A2193715 17.2 78.2 949 197 CNSQ4HNP 17.2 78.2 949 192 CNSQ4HNP 16.8 76.4 258 168 A219391 16.8 76.4 260 104 BE118999 16.8 76.4 396 145 T20362 16.8 76.4 446 24 AN443911 16.8 76.4 446 24 A1761541 16.8 76.4 446 156 AQ332265 16.8 76.4 46 156 AQ332265 16.8 76.4 A64 166 AQ332265 16.8 76.4 A76 178 A76			. ~	78.2	200	24	AI733664	AI733664 an30h03
17.2 78.2 536 39 AW034253, 17.2 78.2 536 39 AW034253, 17.2 78.2 546 24 A1777095 17.2 78.2 612 24 A1777095 17.2 78.2 614 105 BE187570 17.2 78.2 680 174 B57784 17.2 78.2 680 174 B57784 17.2 78.2 680 174 B57784 17.2 78.2 698 168 A2193715 17.2 78.2 949 192 CNSO4HNP 17.2 78.2 949 192 CNSO4HNP 17.3 373 140 C70416 17.7 3 373 140 C70416 16.8 76.4 260 104 BE118999 16.8 76.4 260 104 BE118999 16.8 76.4 396 145 720362 16.8 76.4 432 157 A0443911 16.8 76.4 446 24 A1761541 16.8 76.4 450 138 BF002933 16.8 76.4 464 156 A0332265 16.8 76.4 464 156 A0332265 18.2 76.4 464 156 A0332265 18.3 76.4 464 156 A0332265 18.4 76.4 464 156 A0332265 18.4 76.4 464 156 A0332265 18.4 76.4 464 156 A0332265 18.5 76.4 465 188 A0332265 18.5 76.4 465 188 A0332265 18.5 76.4 465 188 A0332265 18.5 76.4 466 188 A033226			ų,	78.2	524	174	B62582	A0223477 HS 200
17.2   78.2   546   24   A177914     17.2   78.2   579   174   B67515     17.2   78.2   614   105   BE187570     17.2   78.2   614   105   BE187570     17.2   78.2   619   97   AW963886     17.2   78.2   698   168   A2193715     17.2   78.2   698   168   A2193715     17.2   78.2   694   191   CNSOA9DN     17.2   78.2   949   192   CNSOA9DN     17.2   78.2   949   192   CNSOA9NN     17.2   78.2   949   192   CNSOA9NN     17.3   77.3   373   140   C70416     16.8   76.4   296   104   BE118999     16.8   76.4   296   104   BE118999     16.8   76.4   397   91   AW487226     16.8   76.4   432   157   AQ449764     16.8   76.4   446   156   AQ332265     16.8   76.4   464   156   AU38   100wer     16.8   76.4   464   156   AU382040     17.2   AV532040   Arabidopsis thaliana cDNA clone   EB332409     18.2   AV532040   Arabidopsis thaliana cDNA clone   EB33265     18.2   AV532040   AU382040     18.2   AV532040   AU3820323     18.3   AV532040   AU3820323     18.4   AV532040   AU3820323     18.5   AV532040   AV532040     1			٠, ٢	78.7	536	3 6	AW034253	AW034253 EST2778
17.2 78.2 579 174 B67515 17.2 78.2 614 105 BE18750 17.2 78.2 614 105 BE18750 17.2 78.2 619 97 AW965866 17.2 78.2 698 168 AZ177095 17.2 78.2 698 1168 AZ197715 17.2 78.2 904 191 CNSCD9DN 17.2 78.2 904 191 CNSCD9DN 17.2 78.2 904 191 CNSCD9DN 17.2 78.2 949 192 CNSCHNP 16.8 76.4 296 145 T20362 16.8 76.4 396 97 AW943311 16.8 76.4 446 24 A176144 16.8 76.4 446 24 A176144 16.8 76.4 446 156 AQ33265 16.8 76.4 464 156 AQ332265 16.8 76.4 466 16.8 4	27		. 7	78.2	546	24	AI779714	AI779714 EST260
17.2 78.2 614 24 A1777953 17.2 78.2 614 105 BEI87570 17.2 78.2 619 97 AW965686 17.2 78.2 680 174 B57744 17.2 78.2 698 168 A2193715 17.2 78.2 904 191 CNS029DN 17.2 78.2 949 192 CNS04HNP 17.2 78.2 949 192 CNS04HNP 17.2 78.2 949 192 CNS04HNP 17.2 78.2 949 192 CNS04HNP 17.2 78.2 949 192 CNS04HNP 16.8 76.4 296 104 BEI18999 16.8 76.4 396 97 AW943311 16.8 76.4 397 91 AW487226 16.8 76.4 446 24 A1761541 16.8 76.4 446 24 A1761541 16.8 76.4 446 156 A0332265 16.8 76.4 464 156 A0332265 16.8 76.4 464 156 A0332265 ALIGNMENTS  AV532040 Arabidopsis thaliana flower buds Col 14 AV532040 Arabidopsis thaliana flower buds Col AV532040 Arabidopsis thaliana flower buds Col			7	78.2	579	17,	B67515	B67515 T22M1UTI
17.2 78.2 619 97 AW963686 17.2 78.2 680 174 B57784 17.2 78.2 680 174 B57784 17.2 78.2 680 174 B57784 17.2 78.2 904 191 CNSO29DN 17.2 78.2 949 192 CNSO44NP 17.3 373 34 AV31332 16.8 76.4 250 104 BE118999 16.8 76.4 260 104 BE118999 16.8 76.4 396 97 AW943911 16.8 76.4 396 97 AW94391 16.8 76.4 446 24 AT61541 16.8 76.4 446 24 AT61541 16.8 76.4 450 138 BF002933 16.8 76.4 464 156 AO332265 AN532040 Arabidopsis thaliana flower buds Col NAM532040 Arabidopsis thaliana flower buds Col NAM532040 Arabidopsis thaliana flower buds Col AV532040 Arabidopsis ENG34169F 3', mRNA AV532040 Arabidopsis SATA AV532040 Arabidopsis AV532040 Arabidopsis SATA AV532040 Arabidopsis AV532040 Arabidopsis AV532040 Arabidopsis AV532040 Arabidopsis			7.0	7.87	709	4 0	A1///093	BE187570 EST330
17.2 78.2 680 174 B5784 17.2 78.2 698 168 A2193715 17.2 78.2 949 191 CNSO29DN 17.2 78.2 949 192 CNSO4HNP 17.2 78.2 949 192 CNSO4HNP 17.7 3 37 3 140 C70416 16.8 76.4 258 34 AV31332 16.8 76.4 260 104 BE11999 16.8 76.4 396 97 AW48726 16.8 76.4 397 91 AW48726 16.8 76.4 446 24 A1761541 16.8 76.4 446 24 A1761541 16.8 76.4 446 156 AQ33265 16.8 76.4 464 156 AQ332265 16.8 76.4 464 156 AQ332265 ALIGNMENTS  AN532040 Arabidopsis thaliana flower buds COI NAM532040 Arabidopsis thaliana flower buds COI NAM532040 Arabidopsis thaliana flower buds COI AV532040 Arabidopsis AM8NA sequen			ic	78.2	619	97	AW963686	AW963686 EST375
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29-SEP-2000

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Arabidopsis thallana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 490)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yazusa DNA Research Institute Yana 1532-3; Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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//db_xref="taxon:3702"
//clone="App33003.f"
//clone_lib="Arabidopsis thaliana Above-ground organ from two to six-week old plants Columbia"
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    /organism="Arabidopsis thaliana"

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I (bases 1 to 361)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                          The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Klastrazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Clases 1 to 394)

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Contact: Desprez T., Amselem J., Chiapello H., Rouze P., Caboche M., Hofte H.
                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Arabidopsis thaliana flower buds Columbia"
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Route de Saint-Cyr, 78026 Versailles
Emall: Liery@Versailles.inra.fr.
Location/Qualifiers
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and DNA Res. 7, 175-180 (2000)
                                                                                                                                                        The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizuékazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                        /clone_lib="Arabidopsis thaliana aboveground organs two to
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 701676626 A. thaliana, Columbia Col-0, inflorescence-1 Arabidopsis thaliana cDNA clone 701676626, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                      //tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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Tel: 877-577-2733
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/cultivar="Columbia Col-0"
                                                                                                                                                                                                                                                 /organism="Arabidopsis thallana"
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Location/Qualifiers
                                                                                                                                                                                                                                                                             /db_xref="taxon:3702"
/clone="APZ32g06F"
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                                                                                                                                                                                                                                                                                                                        six-week old"
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701676626 A. thaliana,
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90.9%;
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Best Local Similarity 90.9
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/db_xref="taxon:3702"
/clone="701676626"
/clone=11b="A. thaliana, Columbia Col-0, inflorescence-1"
/tissue_1type="inflorescence"
/tissue_type="inflorescence"
/dev_stage"4 - 7 weeks"
/dev_stage"4 - 7 weeks"
/note="Wector: pSPORT: Site_1: NotI; Site_2: SalI; cDNA
library was derived from untreated inflorescence tissue
from Arabidopsis Inhaliana, Columbia Col-0, at 4 - 7
weeks. Plants were grown in 1:1:1 peat
mossyvermiculite/perlite soil at 22 deg. C
- under constant light, and watered with fertilizer. cDNA
synthesis was initiated using a NotI-oligo(dT) primer.
Double-stranded cDNA was blunted, ligated to SalI adaptors
/ digested with NotI, size-selected, and cloned into the
NotI and SalI sites of the pSPORT vector."
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http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 66 row: h column: 08
Seq primer: MI3RPI reverse primer (ABI).
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/lab_host="SOLR (Stratagene)"
/hote="Organ: testis; Vector: pBlueScript SK (Stratagene);
Site_1: EcoR I; Site_2: xho I; Testes dissected from 1-5
day adult y[x] w[67c1]/Y males raised at 25oC. RNA
isolated using Trizol (Life Technologies) and a single
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Laboratory of Cellular and Developmental Biology
NIDDK, Mational Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
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/sex="male"
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/strain="y[*] w[67c1]/Y"
/db_xref="taxon:7227"
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90.9%; Pred. No. 36;
11ve 0; Mismatches 2;
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.ons.fr/Tetraodon.
        CDNA
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
254C22 of library G from Tetraodon nigroviridis, genomic survey
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round of Poly(A)+ selection using Oligotex (Qiagen). CDN
library constructed using Stratagene ZAP-CDNA syntesis
kit. Oligo dT-primed, size fractionated -1-6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
Following a single round of amplification pBlueScript SK
phagemids were mass excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."
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coest-Croflius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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/db_xref="taxon:99883"
/clone="254C22"
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95.0%; Pred. No. 59;
ive 0; Mismatches
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AL190387.1 GI:7828491
GSS; genome survey sequence.
Tetraodon nigroviridis.
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/u.gonism="Medicago truncatula"
/cultivar="genotype A17"
/dultivar="genotype A17"
/dultivar="genotype A17"
/dultivar="genotype A17"
/clone="lb="DSLC"
/clone="lb="DSLC"
/clone=lib="DSLC"
/dev_stage="mixture of cotyledons from five days old plants and leaves obtained from two weeks old plants"
/lab host="E. coli strain SOLR"
/lab host="E. coli strain SOLR cells."
/lab host="E. coli strain SOLR"
/lab host="E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Deborah A. Samac
Contact: Deborah A. Samac
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Fat: 612 625 1243
Fax: 651 649 5058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.

    (bases 1 to 600)

BF006444 600 bp mRNA EST 06-OCT-2000 EST434942 DSLC Medicago truncatula CDNA clone pDSLC-41J15, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fedorova, M., Pierson, B.L., Samac, D.A., Gantt, J.S., Vance, C.P., Gonzales, M.B. and Ellis, L. ESTs from Medicago truncatula leaves and cotyledons
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Intoersity of Minnesota name: M275482e TIGR sequence name:
MTLBASGTK More Information is available at:
http://chrysie.tamu.edu/medicago
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels 0;
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Location/Qualifiers
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BF006254/c
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DEFINITION
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us-09-380-826a-2.rst

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DEMAIL: genome-resertc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Carnindi.p., Nishiyama.y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
Carnindi.p., Nishiyama.y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
Y. and Hayashizaki, Y.
Automated filtration based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kodoka, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shiganco, Y., Shinayawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was cleaved with XhoI and BamHI. Vector: a modified pBluescribt KS(+) after bulk excision from Lambda FLC I." 66~\rm c _20~\rm q _3 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: Sal1: Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                          Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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/db_xref="texon:10090"
/clone="802003zc12"
/clone_lib="RIKEN full-length enriched, 2 cells egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="egg"
/dev_stage="2 cells"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +81-298-36-9013
Fax: +81-298-36-9098
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage=_mixture of cotyledons from five days old plants and leaves obtained from two weeks old plants.
/lab_host="E. col! strain SOLR"
/lab_host="E. col! strain SOLR"
/note="Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from the mixture of cotyledons of five days old plants and leaves of two weeks old plants. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda=ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
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                                                                                                                                                                               Tracheophyta; Spermatophyta;
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                                                                                                                                                    Medicago truncatula
Evaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta,
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
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Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
                                                                                                                                                                                                                                                                                                   Gantt, J.S., Vance, C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: debbys@puccini.crl.umn.edu
University of Minnesota name: M275292e TIGR sequence name:
WTLAU47TK Wore information is available at:
http://chysie.tamu.edu/madicago
Seq primer: Skmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                 1 (bases 1 to 633)
Fedorova, M., Pierson, B.L., Samac, D.A., Gantt, J.S., V
Gonzales, M., B. and Ellis, L.
ESTs from Medicago truncatula leaves and cotyledons
Unpublished (2000)
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Pred. No. 1.2e+02;
O; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pDSLC-40c21"
                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
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                                                            GI:10706529
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Matches 19; Conserv
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                                       ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
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BE581720/c RESULT 11

ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

ACCESSION

TITLE JOURNAL

COMMENT

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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-il. For BAC
Library avallability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
Plate: 642 row: J column: 9
Seq Primer: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 11 others
                                                                                      Mahairas, G.G., Waliace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases I to 674)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NF082E04STIF1034 Developing stem Medicago truncatula cDNA clone NF082E04ST 5', mRNA sequence.
                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 529)
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Pred. No. 1.8e+02;
); Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="Plate=642 Col=9 Row=J"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Unpublished (2000)
Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 529.
Location/Qualifiers
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Best Local Similarity 94.7
Matches 18; Conservative
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AW695022/c
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Eukaryotations stercoralis

Eukaryotations Metazoa: Nematoda; Chromadorea; Rhabditida;

Panagrolaimoidea; Strongyloididae; Strongyloides.

1 (bases 1 to 407)

McCarter, J., Clifton, S., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R. and Wilson, R.

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Porset park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Strongyloides stercoralis"
/strain="Rhabditiform larvae obtained from gerbils"
/db_xref="taxon:6248"
/clone_lib="TBN55TM-SSR"
/clone_lib="TBN55TM-SSR"
/lab_host="XL-1 Blue MRF" (Stratagene); Site_l:
/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site_l:
ECORI; Site_2: Xho!; mRNA was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerbils experimentally infected dogs. cDNA was constructed from experimentally infected dogs. cDNA was constructed and, using adaptors, was cloned unidirectionally into the vector from the Ecori site to the Xho! site. The library has an unamplified titer of 1 x 10E5 ptu/ml and an amplified, undiluted titer of 9 x 10E11 pfu/ml. The average libsert size of the unamplified library is 675 bp (range, 100-1700)."
                                                                                                                       ಧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
The library was constructed by Dr. Thomas Nutman and colleagues of
NIAID, NIH (tnutman@nlh.gov). DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 384.
Location/Qualifiers
                                                                                   BES81720 407 bp mRNA EST 16-AUG-2000 kg51c07.yl TBN95TM-SSR Strongyloides stercoralis cDNA 5' similar WP.T19B10.2 CE16413;, mRNA sequence.
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                                                                                                                                                                                                                                                                Strongyloides stercoralis.
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601101323F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3493829 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:3493829"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
internoal stem segments"
149 c 133 g 203 t
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0
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Pred. No. 1.9e+02;
0; Mismatches 1; Indels 0;
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 674 Std Error: 0.00
Plate: 082 row: E column: 04
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                              /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF082E04ST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Developing stem"
/tissue_type="stem"
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/strain="CZECH II (feral)"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .674
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BE283043
BE283043.1 GI:9159023
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94.78;
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Best Local Similarity 94.7
Matches 18; Conservative
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BE283043
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/organism="Ceratopteris richardii"
/cultivar="Brogn"
/cultivar="Brogn"
/db_xref="texon:49495"
/clone="Cri2_2 Boy"
/clone="Cri2_2 Boy"
/clone_lib="Ceratopteris Spore Library"
/clone_lib="Ceratopteris Spore Library"
/clone_lype="Gametophyte"
/coll_type="Spore"
/dev_stage="20 hours after germination initiation"
/note="Vector: pcMvSPORT6; EST sequence from cDNA library constructed from mRNA isolated from C.
richardii spores that had developed for 20 hours after
their germination had been initiated by white light."
33 a 158 c 214 g 232 t
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Ceratopteris richardii
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Filicophyta;
Filicopsida; Filicales; Pteridaceae; Ceratopteris.
1 (bases 1 to 837)
Chatterjee,A., San Miguel,P., Stout,S.C., Banks,J. and Roux,S.J.
Expressed sequence tags of cDNA clones from a C. richardii library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                             Cri2_7_B04_SP6 Ceratopteris Spore Library Ceratopteris richardii CDNA clone Cri2_7_B04 5', mRNA sequence.
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                                                                                                                         Score 17.4; DB 106; Length 762; Pred. No. 1.9e+02; 0; Mismatches 1; Indels 0;
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Section of Molecular Cell and Developmental Biology
Noniversity of Texas
Biology Building, Room 16, Austin, TX 78712, USA
Tel: 512 471 4238
Fax: 512 232 3402
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providing samples: Gilbert Smith, NIH"
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Plate: Cri2_7 row: B column:
Seq primer: SP6.
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B. subtilis AS2 st

us-09-380-826a-1.rng

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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New isolated pathogenic Leptospira bacterium - useful for, e.g developing products for conferring protective immunity, and for prophylactic or therapeutic treatment
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X77384
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This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainei. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of LS infections. The DNAs and antibodies may also be used for detection and diagnosis of past or present LiS infection.
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          439 G; 314 T; 0 other;
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                    contamination; sea water; detection; flagellum;
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Monitoring of oil contamination of sea water - where oil contamination is evaluated by detection of a microbe having properties from e.g. having no flagellum, being a Gram-negative bacterium, belonging to 'Proteobacteria, gamma subdivision, etc.?
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3; Page 7-8; 15pp; Japanese Claim

The invention relates to a method for monitoring oil contamination of sea water by detecting, in the sea water, a microbe having the following properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium; (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot assimilate glucose as a single carbon source; and (5) it efficiently assimilates at least one of 10-30C n-alkanes. This sequence represents a fragment of the 16S rDNA gene from the microbe of the invention, isolate K3-3.

Sequence 1535 BP; 375 A; 350 C; 496 G; 314 T; 0 other;

ó 246 749 128 188 224 284 306 344 366 tgggggaaacctgaagcagcgcgcgtgaacgaagaaggtcttcggattgtaaagt 404 426 451 486 509 569 629 999 689 104 164 909 Gaps 9 68 ---ctagcggagcgaacgggtgagtaacacgtggtaatcttcc atggtagcttgctaccaggcgtcgagcggcggacgggtgagtaacgcgtgagaatctgcc tecgagtetgggataaettteegaaaggaaagetaataeeggatagteetgttggateae tcattaggcaggaaaaata-----agcagcaatgtgatgatggtacctgcct a--aagcaccggctaactacgtgccagcagccgcggtaatacgtatggtgcaagcgttgt tgggggcaaccctgatccagccatgccgcgtgtgtgaagaaggccttagggttgtaaagc 1 gatcatggctcagaactaacgctggcggcgcgtcttaaacatgcaagtcgagcggggtag catttgtgggggataacttggggaaactcaagctaataccgcataatccctacgggggaa agca--ggggaccttcgggccttgtgcagatggatgagctcgcgtcggattagctagttg gtgaggtaatggctcaccaaggcgacgatcggtagccggcctgagagggtgtccggccac actttcagcagggaaggattcgagttaataccttggagtacttgacgttacctgcag gggctcaacccgtggcctgcacttgaaactacaagtctggagtttgggagggcaagtgg cttgctggctcaaaactgacgctgaggcacgaaagcgtgggtagtagtaacgggattagata aagatttgataggtaaagatttattgcttggagatgagccgcggccgattagctagttg aatggaactgagacacggtccatactcctacgggaggcagcagttaagaatcttgctcaa DB 20; Length 1535; 41; Indels 55.2%; Score 814.6; DB 20; 76.0%; Pred. No. 1.6e-243; iive 0; Mismatches 319; Best Local Similarity 76.0 Matches 1137; Conservative caatac-Query Match 61 69 129 6 105 165 189 225 247 285 307 345 367 405 427 452 487 510 547 570 507 630 299 069 q Op Ωp q ò qq οý q q οp g Dβ qq ç g ò ò ò ŏ ò ογ ò οy ò ò

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Pred. No. 3.7e-243;
0; Mismatches 326; Indels 44;
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                                                                                                                                                                                                                                  The invention relates to a method for monitoring oil contamination of sea water by detecting, in the sea water, a microbe having the following properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium; (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot assimilate glucose as a single carbon source; and (5) it efficiently assimilates at least one of 10-30C n-alkanes. This sequence represents
                                                                                                                                                                                                                                                                                  t least one of 10-30C n-alkanes. This sequence represents the 16s rDNA gene from the microbe of the invention,
                                                                                                                                                                    Monitoring of oil contamination of sea water - where oil contamination is evaluated by detection of a microbe having properties from e.g. having no flagellum, being a Gram-negative bacterium, belonging to Proteobacteria, gamma subdivision, etc.z.
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                                                                                                                                 BIOTECHNOLOGY
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Best Local Similarity 76.2
Matches 1142; Conservative
Monitoring; oil; contamir Gram-negative bacterium;
                  16S rDNA gene;
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                                     Proteobacteria
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                                                            Pectate lyase; polysaccharide lyase; enzyme; pectin degradation; belygalacturonide; detergent composition; hard surface treatment; cellulosic fibre; plant material degradation; recycled waste paper; mechanical paper-making pulp; wine processing; ss.
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Kongsbaek L;
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                                        Bacillus pectate lyase rRNA sequence
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Schnorr
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02-NOV-1998;
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Mannanase; mannan endo-1,4-beta-mannosidase; beta-mannanase; endo-1,4-mannasase; galactcomannan; 1,4-beta-D-mannosidic linkage; mannan; galactcomannan; galactcomannan; cellulosic fibre; synchetic fibre; yarn; fabric; printing paste; thickener; viscosity; plant material degradation; recycled waste paper; paper making pulp; quar; locust bean gum; mannan-containing food; coffee extract; cleaning composition; machine washing; hard-surface cleaner; 16S RNA; dishwashing; oral; dental; contact lens; body-care composition; fabric softener; oil well drilling; subterranean formation fracture; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the 16S RNA sequence of Bacillus sp. AA112. This bacterium encodes a mannanse enzyme (also known as mannan endo-1,4-beta-mannosidase, beta-mannanase, or endo-1,4-mannanase). The mannanase hydrolyses galactomannans. Specifically, mannanases hydrolyse 1,4-beta-D-mannosidic linkages in mannans, galactomannans, palactomannans, preparations containing it, are used to improve properties of cellulosic or synthetic fibres, yarn or (non)woven fabrics (removal of mannan-based
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                              ccgcccgtcacaccacctgagtggggagcacccgaagtggtctttgttaaccgta-agga
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sizes or printing pastes). They are also used to degrade or modify plant materials (particularly recycled waste paper, paper making pulps, or material containing quar or locust bean gums (thickeners), or to reduce viscosity of mannan-containing foods or feeds). The mannanases are also used to process coffee extracts (to inhibit gel formation); in cleaning compositions (for machine washing of fabrics, as hard-surface cleaning compositions (for shine washing, also in oral, dental, contact lens or body-care compositions) where they remove mannan-containing soils and prevent binding of some soils to cellulosics; and in fabric softeners. They can also be used in oil well drilling to fracture
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                          Monitoring of oil contamination of sea water - where oil contamination is evaluated by detection of a microbe having properties from e.g. having no flagellum, being a Gram-negative bacterium, belonging to Proteobacteria, gamma subdivision, etc. 2
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Score 808.4; DB 20; Pred. No. 1.3e-241; 0; Mismatches 316;

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                                                                                                                                                                                                                                                       16S rDNA gene fragment from marine bacterium, isolate
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The invention relates to a method for monitoring oil contamination of sea water by detecting, in the sea water, a microbe having the following properties: (1) it has no flagellum: (2) it is a Gram-negative bacterium; assimilate glucose as a single carbon source; and (5) it efficiently assimilates at least one of 10.30c n-alkanes. This sequence represents a fragment of the 16s rDNA gene from the microbe of the invention, isolate Wf-2.
                                                                                                                                                                                                                     Monitoring of oil contamination of sea water - where oil contamination is evaluated by detection of a microbe having properties from e.g. having no flagellum, being a Gram-negative bacterium, belonging to
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   Proteobacteria
                             JP11243967-A.
                                                                                              04-MAR-1998;
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                                                              14-SEP-1999
                                                                                                                                                                                                                                                                                                   Claim
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Taxane; paclitaxel; plant; bacteria; mutation; cancer; 16S

Bacillus cereus

WO9932651-A1

compounds

paclitaxel

English

Disclosure; Fig 8E; 93pp; Production of taxane and

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Gagne M, DEV INC

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(BCMB-) BCM

WPI; 1999-418940/35

97US-0995960 98WO-CA01150

22-DEC-1997;

18-DEC-1998;

B. cereus BCM 4 partial 16S rRNA gene sequence

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The invention relates to a new method for the production of taxane and paclitaxel compounds that comprises culturing bacteria isolated from a plant species of Taxus or bacteria produced by mutating the isolated bacteria. The methods can be used for the production of taxanes such as paclitaxel, 10-deacetylcephalomannine, 7-epitaxol, 10-deacetyl-7-epitaxol, 7-epicephalomannine, baccatin III, 10-deacetyl-baccatin III, cephalomannine, taxanine, delta-barcoploxy taxagifine, 9-acetyloxy taxusin, 9-hydroxy taxane and paclitaxel compounds can be used for the treatment of cancers. The methods can provide for the production of taxanes and paclitaxel at a concentration of 1-25 mu g/l.
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strain DSM 8721. This is a reference standard for isolation o
closely related strains (more than 92% sequence identity, or
preferately more than 93% identity of IGS ribosomal DNA) which
produce thermostable alkaline endo-1,4-beta-D-xylanase, which
is useful in paper production and pulp bleaching. The strain
itself produces such a xylanase.
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    useful in paper

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Williams DP;
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Iverson S, Jones BE, Quax WJ, Van
Van der Kleij WA, Van Solingen P,
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his sequence represents the 16S rRNA gene of Pseudomonas cepacia
train KKOl. Fragments of the nucleic acid sequence (see T01872-T02316)
re useful as primers and probes for the specific detection of P.cepacia
train KKOl.
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equence 1526 BP; 382 A; 352 C; 486 G; 306 T; 0 other;
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The invention relates to a method for monitoring oil contamination of sea water by detecting, in the sea water, a microbe having the following properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium; (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot assimilate glucose as a single carbon source; and (5) it efficiently a similates at least one of 10-30C n-alkanes. This sequence represents isolate TE-9.
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Proteobacteria; glucose; carbon source;
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Best Local Similarity 75.6%;
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The invention relates to a method for monitoring oil contamination of sea water by detecting, in the sea water, a microbe having the following properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium; (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot assimilate glucose as a single carbon source; and (5) it efficiently assimilates at least one of 10-30C n-alkanes. This sequence represents a fragment of the 16S rDNA gene from the microbe of the invention, isolate K2-1.
                                                           Monitoring of oil contamination of sea water - where oil contamination is evaluated by detection of a microbe having properties from e.g. having no flagellum, being a Gram-negative bacterium, belonging to Proteobacteria, gamma subdivision, etc.?
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Gram-negative bacterium; Proteobacteria; glucose; carbon source;
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Novel bacterial strain ADP (ATCC 55464), isolated from atrazine-contaminated soil, is capable of degrading s-triazine cpds., including atrazine. In an attempt to identify the strain, the 165 ribosomal RNA sequence (T18760) was compared to that of Escherichia coli (T18759), Pseudomonas citronellolis ATCC 15674 (T18761-63), and Pseudomonas aeruginosa (T18764), Pseudomonas testosteroni (T18765) and Pseudomonas cepacia (T18766). It was concluded that ADP is closely related to, but distinct from, P. citronellolis and P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biologically pure culture of atrazine-degrading Pseudomonas - unto detoxify atrazine, e.g. in soil, at a wide variety of concus
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bioremediation; s-triazine; herbicide; ss.
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Atrazine; pesticid

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MPI; 1996-208726/2;

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Coll (T18759); pseil

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COLL (T18750); pseil

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54.4%; Score 803.8; DB 17; 60.2%; Pred. No. 3.6e-240; ive 216; Mismatches 343;

Query Match 54.4%; Sc Best Local Similarity 60.2%; Pr Matches 897; Conservative 216;

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δλ	635	tgtagcggtgaaatgcgtagatatctggaggaacaccagtggcgaa	
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οy	755	taatccacgccctaaacgttgtctaccagttgttgggggttttaaccctca	
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Patent No. 5874291
Patent No. 5874291
APPLICANT: Herwig, Russell P. APPLICANT: Bielefeldt, Angela R. APPLICANT: Stensel, H. Dayid
APPLICANT: Stensel, H. Dayid
APPLICANT: Stensel, H. Degradation of Environmental Toxins by a TITLE OF INVENTION: Degradation of Environmental Toxins by NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Christensen O'Connor Johnson and Kindness PLLC 1420 Fifth Avenue, Suite 2800
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US-08-632-470-41
US-08-632-470-29
US-08-632-470-45
US-08-632-470-47
US-08-632-470-47
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682 8100
TELEFAX: (206) 224 0779
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ZIP: WA 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, N
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/246,865
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: nucleic acid
DESCRIPTION: "16S ribosomal DNA"
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TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Christens
STREET: 1420 Fifth A
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-114-695A-6
US-08-129-810A-27
US-08-875-445-21
US-08-632-470-49
US-08-642-229A-2
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US-09-248-528-3
US-08-114-695A-1
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US-08-757-653-160
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US-08-995-960-1
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US-08-632-470-35
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                                                         Length 1536;
                                                                                         Indels
                                                     Score 814.2; DB 2;
Pred. No. 4.8e-284;
0; Mismatches 343;
                                                   Query Match
Best Local Similarity 74.7%;
Matches 1113; Conservative
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TACCCACCTTTGACATGGCAGGAACTTACCAGAGATGGTTTGGTGCTCGAAAGAGAACCT 1033
                                  cggtgacaaaccggaggaaggcggggatgacgtcaaatcctcatggcctttatgtccagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,126
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TITLE OF INVENTION: ALKALI-TOLERANT XYLANASES
NUMBER OF SEQUENCES: 20
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Van Der Kleij, Wilhelmus A.
Herweijer, Margaretha A.
Van Beckhoven W.C., Rudolf F.
Quax, Wilhelmus J.
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NAME: Wurashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-0057.00
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Williams, Diane P.
Iverson, Sara
Farrell, Roberta L.
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Patent No. 6140095
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 29-DEC-1995
CLASSIFICATION: 425
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NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                            37;
                                                                                                                                                                      Length 1521;
                                                                                                                                                                                             Indels
                                                                                                                                                                     54.5%; Score 805.4; DB 3; 76.9%; Pred. No. 7.3e-281; ive 0; Mismatches 292;
                                                                                                                  ORGANISM: Bacillus sp.
INDIVIDUAL ISOLATE: DSM 8721
                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
                                                                                                                                                                                            Matches 1097; Conservative
                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                   Similarity
                                                                                                          ORIGINAL SOURCE:
                                                                                                                                        US-08-501-126-20
                                                                                                                                                                        Query Match
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                                                                                940 tgggcttgaca----tggatctgaatcatgtagagatatatgagccttcgggcagattc
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COMPUTER: IBM PC COMPATIBLE
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/114,695A
FILING DATE: 31-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mandelbaum, Raphael T.
APPLICANT: Wackett, Lawrence P.
TITLE OF INVENTION: DEGRADATION OF
TITLE OF INVENTION: WATER
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SCHWEGMAN, LUNDBERG
STREET: 3500 IDS CENTER
CITY: MINNEAPOLIS
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                                                                                                                                                       Length 1536
                                                                                                                                                                           Indels
                                                                                                                                                      Query Match 54.4%; Score 803.8; DB 1; Best Local Similarity 60.2%; Pred. No. 2.8e-280; Matches 897; Conservative 216; Mismatches 343;
 600.268US1
                                                                                                                  ORGANISM: Pseudomonas testosteroni
REFERENCE/DOCKET NUMBER: 6
TELECOMOUNICATION INFORMATION
TELEBHONE: 612-339-0331
TELEFAX: 612-339-3061
                                  INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 base pairs
TYPE: nucleic acid
                                                                             single
                                                                TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
MOLECULE TYPE: rRNA
ORIGIANL SOURCE:
                                                                                                                           US-08-114-695A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman,
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT

US-08-995-960-2

Sequence 2, Application US/08995960

Patent No. 6030818

GENERAL INFORMATION:

APPLICANT: PAGI, Michel

APPLICANT: BOISSINOT, Maurice

APPLICANT: HILLE, Marie-Claude

APPLICANT: HILLE, Marie-Claude

APPLICANT: GAGNI, Martin

TITLE OF INVENTION: BACTERIAL MASS PRO

TITLE OF INVENTION: OF TAXANES AND PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 160, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
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                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                             8; DB 3;
1.4e-279;
                                                                                                                                                                                                                                              0; Mismatches 322;
SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,960
FILING DATE: 22-DEC-1997
CLASSIFICATION 2435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            54.3%; Score 801.8; 75.3%; Pred. No. 1.46
                                                                                       34,235
                                                                                              REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                      75.3%;
                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
                                                                             NAME: RESNICK, David S
REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                    Best Local Similarity 75.3
Matches 1134; Conservative
                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: rRNA
                                                                                                                                                                                                   US-08-995-960-2
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                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                        54.3%; Score 801.6; DB 2; 75.3%; Pred. No. 1.7e-279; .ive 0; Mismatches 324;
                          Suite 2200
                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 60,027
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415,397-8338
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CARRACTERISTICS:
LENGTH: 1555 base pairs
TYPE: nucleic acid
STRANDEDNESS: aduble
                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN RELEASE #1.0, CURRENT APPLICATION DATA: FILING DATE:
                                                        America
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LL
STREET: 220 Montgomery Street,
CITY: San Francisco
STATE: California
COUNTRY: United States Of Ameri
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US-08-757-653-160
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Best Local Similarity 75.3
Matches 1134; Conservative
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US-09-248-528-2
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; Patent No. 6153415
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APPLICANT: Padmakumar, Rugmini
APPLICANT: Kim, Sang H
TITLE OF INVENTION: Method for Producing Amide Compounds Using
TITLE OF INVENTION: Hydratase from a Thermophilic Bacillus
FILE REFERENCE: MSU 4.1-401
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APPLICANT: Coriel, Patrick J
APPLICANT: Padmakumar, Rugmini
APPLICANT: Padmakumar, Rugmini
APPLICANT: Ann, Sang H
TITLE CANT: Min, Sang H
TITLE OF INVENTION: Hydratase from a Thermophilic Bacillus
FILE REFERENCE: MSU 4.1-401
CURRENT APPLICATION NUMBER: US/09/248,528C
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 60/083,485
SERIER APPLICATION NUMBER: 60/083,485
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1517
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llarity 75.0%; Pred. No. 3.7e-276;
Conservative 0; Mismatches 326;
                                                                                                                                                                                       LOCATION: (1)..(1517).
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: 226929
DATABASE ENTRY DATE: 1998-07-02
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Best Local Similarity
Matches 1128; Conserv
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FEATURE:
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53.5%; Score 789.8; I
Best Local Similarity 75.0%; Pred. No. 3.2e-
Matches 1124; Conservative 0; Mismatches
                                                              TYPE: DNA
ORGANISM: Bacillus pallidus
FEATURE:
NAME/KEY: FRNA
LOCATION: (1)..(1516)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: 226930/GenBank
DATABASE ENTRY DATE: 1997-05-14
 US/09/248,528C
CURRENT APPLICATION NUMBER: US/09/248, CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 60/083, 485
EARLIER FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Wackett, Lawrence P.
TITLE OF INVENTION: DEGRADATION OF S-
TITLE OF INVENTION: WATER
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHWEGMAN, LUNDBERG & WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3500 IDS CENTER
CITY: MINNEAPOLIS
STATE: MN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/08114695A
; Patent No. 5508193
; GENERAL INFORMATION:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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MEDIUM TYPE: Floppy
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US-08-114-695A-1
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TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
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STREET: 220 Montgomery Street, St
CITY: San Francisco
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Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
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COUNTRY: United St
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,695A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
ATTORNEY-AGENT INFORMATION:
NAME: WUGTING, ANN M.
REGISTRATION NUMBER: 600.268US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPHONE: 612-339-031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Escherichia coli
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ORIGINAL SOURCE:
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TOPOLOGY: lir
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                 gactigctggctcaaaactgacgctgaggcacgaaagcgtgggtagtaacgggattaga
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Patent No. 5508193
GERBEAL INFORMATION:
APPLICANT: Mandelbaum, Raphael T.
APPLICANT: Wackett, Lawrence P.
TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES I
TITLE OF INVENTION: WATER
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A
STREET: MINNEAPOLIS
STATE: MN
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                                                                                                                                                                                                                                                                                    Length 1542;
                                                                                                                                                                                                                                                                             Query Match 52.8%; Score 780; DB 2; Length 15
Best Local Similarity 74.5%; Pred. No. 1.1e-271;
Matches 1116; Conservative 0; Mismatches 340; Indels
                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
                                                                                          ATTORNEY/AGENT INFORMATION:

NAME: Ingolia Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02565

TELECOMMUNICATION INFORMATION:

TELEPAN: (415) 39-838

INFORMATION FOR SEQ ID NO: 158:

SEQUENCE CHARACTERISTICS:

LENGTH: 1542 base pairs

TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-757-653-158
           Floppy disk
COMPUTER READABLE FORM:
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1166 ccagggccacacacgtgctacaatggccgatacagagggtcgccaactcgcaagagggag
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Sequence 1, Application US/08995960
Fatent No. 6030818
Patent No. 6030818
PPLICANT: PAGI, Michel
APPLICANT: EANDRY, Nathalie
APPLICANT: BOISSINOT, Maurice
APPLICANT: HILE, Marie-Claude
APPLICANT: HARVEY, Mario
APPLICANT: GAGNI, Martin
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                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  Length 1474;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/114,695A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Query Match 52.8%; Score 779.8; DB 1; Best Local Similarity 60.5%; Pred. No. 1.3e-271; Matches 876; Conservative 201; Mismatches 328;
                                                                                                                                       NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPHONE: 512-339-031
INFORMATION FOR SED ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas cepacia
                                                                                                                                                                                                                                              LENGTH: 1474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: rRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                          US-08-114-695A-8
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                                                                                                                                                                                                                                                                                                                                                                                            Length 1556;
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TITLE OF INVENTION: BACTERIAL MASS PRODUCTION
TITLE OF INVENTION: OF TAXANES AND PACLITAXEL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Dike, Bronstein, Roberts & Cushman,
STRET: 130 Water Street
CITY: Boston
STAFE: MA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                        52.7%; Score 778.4; DB 3; 74.7%; Pred. No. 4.3e-271; tive 0; Mismatches 336;
                                                                                                             MEDIUM TITE: DISRELLE
COMPUTER: DISRELLE
COMPUTER: TIBM COMPACTIBLE
OPERATING SYSTEM: Windows
SOFTWARE: FASLSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,960
FILING DATE: 22-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: RESMICK, David S
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 1826/47986
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1556 base pairs
TYPE: nucleic acid
                                                                            COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: rRNA
US-08-995-960-1
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Best Local Similarity
Matches 1095; Conserv
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                                                                      gcggatttgtaagtcaggtgtgaaaactgcgggctcaacccgtggcctgcacttgaaact
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                                                                                                AGAAGAAGCACTGGCTAACTCTGTGCCAGCAGCGGGTAATACAGAGAGTGCAAGCGTT
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                                                   APPLICANT: MABILAT, CLAUDE
APPLICANT: MABILAT, CLAUDE
APPLICANT: RAOULT, DIDIER
TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
TOWNERS OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC Compatible
OPPRATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 772.6; DB 2;
Pred. No. 5.2e-269;
0; Mismatches 337;
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
TELEPHONE: (703)-836-5787
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
          Sequence 53, Application US/08632470 Patent No. 5976791 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: DNA (genomic)
US-08-632-470-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 52.3%;
Best Local Similarity 74.1%;
Matches 1082; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1484 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                               USA
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                                                                                                                              WOESSNER,
                                              GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: MANGELDAUM, Raphael T.
APPLICANT: Wackett, Lawrence P.
TITLE OF INVENTION: DEGRADATION OF S-T
TITLE OF INVENTION: WATER
NUMBER OF SEQUENCE: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHWEGMAN, LUNDBERG & WOE
STREET: 3500 IDS CENTER
CITY: MINNEAPOLIS
STATE: MI
                                                                                                                                                                                                                                 SOLTWARD.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,695A
FILING DATE: 31-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                   Sequence 6, Application US/08114695A Patent No. 5508193
                                                                                                                                                                                                                                                                                      NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-3061
TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                          FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1518 base pairs
                                                                                                                                                                                                                                                                                                                                      TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                  RESULT 13
US-08-114-695A-6
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           TGGGGGATAACTTGGGGAAACCCAAGCTAATACCGCATACGACCTACGGGTGAAAGG---
                                                                                                                                                                                   STRAINS
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CATARRHALIS
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Pred. No. 1.7e-267;
0; Mismatches 322;
                                                                                                                Sequence 27, Application US/08299810A
Patent No. 5721097
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rossau, Rudi
APPLICANT: Van Heuverswyn, Hugo
TITLE OF INVENTION: DETECTION OF BRANHAMELLA
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/299,810A
FILING DATE: 01-SEP-1994
CLASSIFTCATION: 435
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: H11son, Randall A.
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.70-US-WO
TELECHMUNICATION INFORMATION:
TELEPHONE: 612-332-9081
                                                                                                                                                                                                               ADDRESSEE: Merchant & Gould STREET: 3100 No. 5721097west Center CITY: Minneapolis STATE: MN COUNTRY: USA ZIP: 55402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Branhamella catarrhalis
                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 52.0%;
Best Local Similarity 75.1%;
Matches 1075; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1485 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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CLONE: 16S rRNA Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOLOGICAL NAME: Pectinatus
                                                                                                                                                                                  APPLICANT: Kanta SAKAMOTO
TITLE OF INVENTION: DETECTION OF THE GENUS
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                          Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                    inch, 1.44
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                                                                                                                                                ; Sequence 21, Application US/08875445
; Patent No. 5869642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , CECLOGY: linear
, MOLECULE TYPE: genomic DNA
, ORIGINAL SOURCE:
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US-08-875-445-21
                                                                                                                                                                                                                                                                            ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETLE, 3.5
CAMPITER: IBM COMPATIBLE
MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21:
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FILING DATE: July 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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74.7%;
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Best Local Similarity 74.7
Matches 1126; Conservative
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ADDRESSEE: Wenderoth,
STREET: 805 Fifteenth
CITY: Washington
STATE: D.C.
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28-JAN-2000 clone LERAP36, DNA

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Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaeae, Arabidopsis.
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Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utter Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thallana and identification of sequence-based
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LERA Arabidopsis thaliana genomic
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Pred. No. 1.3e-123;
0; Mismatches 140;
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Contact: Xiaoying Lin
The Institute for Genomic Research 9712 Medical Center Dr., Rockville,
Fat: 301 838 0200
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For additional information, see
Seq primer: TR
Class: shotgun.
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                   Spermatophyta;
Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta,
Bagnoliophyta; eudloctyledons; core eudicots; Rosidae; eurosids II.
Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 800)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,
Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                         Contact: Xiaoying Lin
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: attetigr.org/tdb/at/at.html
For additional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
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1. .800
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Salanoubat,M., Choisne,N., Artiguenave,F., Brottier,P., Wincker,P., Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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-----aagcaccggctaactacgtgccagcagcggtaatacgtatggtg
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                             attgtaaagttcattaggcaggaaaaataagcagcaatgtgatgatgtacctgccta--
                                               GTTGTAAAGCTCTTTCGCAAGGAAGAAACTTACTTTCTAATAAAGAGTGAGGCTGACG
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Submitted (25-JUN-1999) Genoscope - Centre B
BP 191 91006 EVRY cedex - FRANCE (E-mail : Web : www.genoscope.cns.fr)
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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LERAP36TF LERA Arabidopsis thaliana genomic clone LERAP36, DNA
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Pred. No. 2.5e-118;
0; Mismatches 156; Ir
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/db_xref="taxon:3702"
/clone_lib="TAMU"
/clone="Tl1H14"
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ilarity 77.2%;
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Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 746)

Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Ling,F., Creasy,T. and Fraser,C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                              /clone="LERAP36"
/clone_lb="LERA"
/note="Organ: Legh; Vector: pHOS1; Total genomic DNA was
sheared to 0.9-1 Kbp before ligation."
153 c 225 g 159 t l others
                                                                     polymorphisms
Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Exx: 301 838 0208
Exx: 301 838 0208
Exx: 502 pational information, see http://www.tigr.org/tdb/at/at.html
Seq primer: TF
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                          84 agtaacacgtggtaatcttcctccgagtctgggataactttccgaaaggaaagctaatac 143
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Pred. No. 1.8e-112;
0; Mismatches 181;
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1. .746
/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
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73.0%;
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534; Conservative
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Magnollophyta; endicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 741)
Buell.C.R., Lin.X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Arabidopsis thallana and identification of sequence-based
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: atétigr.org
For additional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
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LERAO33TR LERA Arabidopsis thaliana genomic clone LERAO33, DNA
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/note="Organ: Leaf; Vector: pHOS1; Total genomic DNA sheared to 0.9-1 Kbp Defore ligation."
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Pred. No. 9.5e-111;
0; Mismatches 169; Indels
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/db_xref="taxon:3702"
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Best Local Similarity 74.6
Matches 525; Conservative
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bugaryota; Viridiplantae; Embryophyta; Core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 757)
Buellic.R., Lin.X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T.,
Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thallana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: at@tigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
                                                                                                                                                                                                                                                                                                                                                                                GSS 28-JAN-2000 thaliana genomic clone LERAO34, DNA
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346
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/strain="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LERAO34"
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Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0200
Fax: 301 838 0208
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LERAO34TR LERA Arabidopsis
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Class: shotgun
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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c clone T27K4, DNA
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                                                                                                                                                                       451 GACGGTATCTGGGGA----ATAAGCATCGGCTAACTCTGTGCCAGCAGCGGGTAAT
                                                                                                                                                                                                                                                                                            310 tectaegggaggeageagttaagaatettgeteaatgggggaaaceetgaageagegaeg
              Total genomic
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/clone_lib="LERA"
/note="Organ: Leaf; Vector: pHOS1: To
sheared to 0.9-1 Kbp before ligation.
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T27K4TR TAMU Arabidopsis thaliana genomic
                                                                                                        Score 378.8; DB 165
Pred. No. 3.2e-109;
0; Mismatches 167;
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llarity 74.6%;
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Best Local Similarity
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           A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3 Update 13 Update 1997) Other GSSs: T27K4TF Contact: Steve Rounsley
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Pred. No. 1.6e-108;
0; Mismatches 155; Indels
                                                                                                                                   USA
                                                                                                    Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0200
Email: rounsley@tigr.org
Seg primer: M3 Reverse
                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
                                                                                                                                                                                                        High quality sequence stop: 676.
Location/Qualifiers
                                                                                                                                                                                                                                                     /strain="Columbia"
/db_xref="taxon:3702"
/clone="T27K4"
                                                                                                                                                                                                                                                                                                    /sex="hermaphrodite"
1 (bases 1 to 676)
Rounsley, S.D., Field, C.E.,
                                                                                                                                                                                                                                                                                         /clone_lib="TAMU"
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Best Local Similarity 76.2%;
Matches 515; Conservative
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 693)

Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liandy, F., Creasy, T. and Fraser, C.M.
Arabidopsis thallana and identification of sequence-based
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//strain="Landsberg erecta"
//db_xrref="taxon:3702"
//clone="LERA19"
//clone="LERA"
//clone="Lera"
//orlone="Corgan: Leaf; Vector: pHOS1; Total genomic DNA was sheared to 0.9-1 Kbp before ligation."
221 c 157 g 178 t lothers
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                                                                              gtcgccaactcgcaagaggagctaatctctaaaagtcggtcccagttcggattggggtc 1263
aagcaccggctaactacgtgccagcagccgcggtaatacgtatggtgcaagcgttgttcg 512
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LERAJ19TR LERA Arabidopsis thaliana genomic clone LERAJ19, DNA
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illarity 77.2%; Pred. No. 2.2e-103;
Conservative . 0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymorphisms
Uppublished (2000)
Contact: Alaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
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Arabidopsis thaliana

Busaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids II;

Magnoliophyta; Brassicaceae; Arabidopsis.

E (bases I to 676)

E (conair to 676)

E (along, C., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,

Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.

Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.

Reldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.

Arabidopsis thaliana and identification of sequence-based polymorphisms

AL Unpublished (2000)

Contact: Xiaoying Lin

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 02008

Fax: 301 838 02008
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Location/Qualifiers

1. 676

/organism="Arabidopsis thaliana"
/strah="Laxon:3702"
/clone="LENJRS"
/clone="LENJRS"
/clone="Lends"
/clone="Lends"
/clone="Corgan: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4°7 Kbp before ligation."
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For addtional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
Seq primer: TF
Class: shotgun.
                                                                                                                                                                                                                                                                                          A GSS 28-JAN-2000
thaliana genomic clone LERJR28, DNA
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                                                                             cggtaatccacgccctaaacgttgtctaccagttgttgggggttttaaccc--tcagtaa 810
                                        aacctcacctgggcttgacatggatctgaatc-atgtagagatatatgagccttcggg--
TTCCGGTGGAGCGGTGAAATGCGTAGAGATCGGAAAGAACACCAACGGCGAAAGCACTCT
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LERJR28TF LERG Arabidopsis
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AQ969911
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Arabidopsis thaliana
Arabidopsis thaliana
Bustayota; Viridiphantae; Embryophyta; Tracheophyta; Spermatophyta;
Bustayota; Viridiphantae; Embryophyta; Tracheophyta; Bustayota; Viridiphantae; Embrasicaceae; Arabidopsis.

I (bases 1 to 659)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liang, F., Creasy, T., and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                     9
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LERJR90TF LERG Arabidopsis thaliana genomic clone LERJR90, DNA
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                                            Gaps
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Score 359.6; DB 165; Lengt
Pred. No. 4e-103;
0; Mismatches 149; Indels
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AQ969996.1 GI:6797697
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Unpublished (2000)

Contact: Xiaoying Lin

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
7 = 1301 838 0200
Fax: 301 838 0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 CTAACTCCAAAAACCCGTCCTCAGTTCGGATTGCAGGCTGCAACTAGCCTGCATGAAGCC
                                                                                                                                                                                                                                                                                                                     DB 165; Length 659;
                                                                                                                                                                                /strain="Landsberg erecta"
/db_xref="taxon:3702"
/clone="lbERGR90"
/rolone_lbERGR"
/note="Organ: Leaf; Vector: pUC19JK; Total/, sheared to 0.4-0.7 kbp before ligation."
                                                                                                                                                                                                                                                                                                                    Score 356.6; DB 165; Lengtl
Pred. No. 3.6e-102;
0; Mismatches 139; Indels
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                                                                                                                                           Location/Qualifiers
1. .659
/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                   Query Match 24.1%;
Best Local Similarity 77.3%;
Matches 497; Conservative
                                                                                                                                                              source
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/organism="Lycopersicon esculentum"
/cultiva="TA496"
/db_xref="taxon:4081"
/clone="clath4113"
/clone="Lib="tomato fruit red ripe, TAMU"
/clone="Lib="tomato fruit red ripe, TAMU"
/clone="tope" red ripe (7-20 days post-breaker)"
/dev_stage="red ripe (7-20 days post-breaker)"
/dev_stage="tope" red ripe (7-20 days post-breaker)
/dev_stage (first sign of lycopene accumulation on the breaker stage (first sign of lycopene accumulation on the breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; educotyledons; core eudicots; Asteridae; euasterids 1: Solanales; Solanaceae; Solanum; Lycopersicon.

I (bases 1 to 677)
Alcala, J., Vebalov, J., Whiter, R., Mattern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M. B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J. Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
EST298662 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA AW221851
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llarity 77.0%; Pred. No. 7.8e-101;
Conservative 0; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Trel: 864 656 4366
Fax: 864 656 4293
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1 677
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                                                                                                                                                                                                      Lycopersicon esculentum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-607-1999) to the DDBJ/EMBL/GenBank databases.
Submitted (10-607-1999) to the DDBJ/EMBL/GenBank databases.
Masahira Hattori, RIKEN Genomic Sciences Center(GSC) c/o Kitasato
University; 1-15-1 Kitasato, Saqamihara 228-8555, Japan
(E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:042-778-9923,
Fax:042-778-9924)
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1 (bases 1 to 616)
Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T., Park,H.-S., Yada,T., Watanabe,H. and Sakkki,Y.
Published Only in DataBase (1999) In press
2 (bases 1 to 616)
Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.
Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.
                                                                                                                                                     361 GGCCGGGACAAAAGGGTCGCGGATCCCGCGGAGGTGAGCTAACCCCAAAAACCCGTCCTCAG
                                                                                                     ttcggattggggtctgcaactcgaccccatgaagtcggaatcgctagtaatcgcggatca
                                                                                                                                                                                                                      ggccgatacagagggtcgccaactcgcaagagggagctaatctctaaaagtcggtcccag
                                                                                                                             421 TTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCGCCGGTCA
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Pred. No. 2.8e-100;
0; Mismatches 119; Indels
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                                                                                                                                                                                                                                                                        600 ACTGACTGGAGTGGAACAACAAGGTAGCGGTACTGGA 639
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Homo sapiens
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/db_xref="taxon:9606"
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ilarity 78.9%;
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Best Local S:
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Eukaryotta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 6/75)
Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thallana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: at@tigr.org
For additional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
Seg primer: TF
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: Leaf; Vector: pHOS1; Total genomic DNA was sheared to 0.9-1 Kbp before ligation."
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                                                                                                                                            1107 ctgccggtgacaaaccggaggaaggcggggatgacgtcaaatcctcatggcctttatgtc 1166
                                                                                                                                                                                                                                    1167 cagggccacacacgtgctacaatggccgatacagagggtcgccaactcgcaagagggagc 1226
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LERAJ19TF LERA Arabidopsis thaliana genomic clone LERAJ19, DNA
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                                               496 CGFGAGACAGGFGCTGCAFGGCTGTCGTCAGCTCGTGTTGFGAAATGTTGGGTTTAAGTCC
                                                                                                                                                                                                                                                                    Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
11: 301 838 0200
Fax: 301 838 0208
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/db_xref="taxon:3702"
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/clone_lib="LERA"
/note="Organ: Leaf
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AQ956297.1 GI:6783998
GSS.
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Arabidopsis thaliana
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Unpublished (2000)
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/dev_scage="Adult"
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//note="Organ: testis: Vector: pucl8; Site_1: Smal; Site_2:
//note="Organ: testis: Vector: pucl8; Site_1: Smal; Site_2:
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//note="Organ: testing devived 
                                                                                                                                                                                              Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=0v0-TT0009-191
199-056-b02&t3=1999-11-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 659.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 659;
                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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     (7), 3491-3496
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Pred. No. 3.6e-98;
0; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .659
/organism="Homo sapiens"
     6
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/clone_lib="TT0009"
  U.S.A.
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ilarity 74.4%;
Conservative
                                                                                                                                                                            Tel: +55-11-2704922
     Natl. Acad.
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldoman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW833978 659 bp mRNA EST 18-MAY-2000
QVO-TT0009-191199-056-b02 TT0009 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                     Gaps
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                                                                                                    Length
                                                                                               Score 346.8; DB 165; Lengt
Pred. No. 4.7e-99;
0; Mismatches 162; Indels
  124
  5
  222
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AW833978.1 GI:7927952
                                                                                               23.5%;
73.8%;
     O
                                                                                                                                                  Matches 484; Conservative
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  a
  176
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                              The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 153-3. Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                     Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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Brassicales; Brassicaceae; Arabidopsis.
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OM nucleic - nucleic search, using sw model

March 27, 2001, 08:22:56; Search time 207.51 Seconds (without alignments) 39.827 Million cell updates/sec Run on:

US-09-380-826A-2 22 Perfect score:

1 tgttggatcacaagatttgata 22 Sequence:

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 480022 seqs, 187831343 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_36:\* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Maize acetyl CoA c EcoRI fragment of M. leprae gyrA pre A3 maize ACCase cD Human secreted pro B. burgdorferi ant Acetyl-CoA-carboxy Human secreted pro Leptospira rRNA ge L. fainei nucleoti L. fainei nucleoti Maize male fertili Description SUMMARIES V58901 V58897 V58896 T90543 V84598 V59636 X61757 T171111 T39904 T49916 T49816 C42933 ΩÏ Query Match Length DB 22 16.8 16.2 16.2 16.2 16.2 16.2 16.2 Score Result 4 7 7 10 10 11 11 12 ٠ ي

Maize acetyl CoA c Maize ACCase enzym Maize acetyl CoA c Potato pollen cell Human gene express	Human hypoxia resp EST clone HK650. Adenovirus pACTSG2 Adenovirus SCAR.RG	Encodes fibrinogen Adenovirus pACSG2S Callosellasma rhod Human coxsackietir	DNA encounty a bac Black Creek Canal Human Coxsackievir Enterococcus faeca Genomic DNA encodi Sh2-mRev6 gene (s Sh2-mRev6 gene (s Sh1-mrken-2 gene wa Wild-type shrunken	Human type IV coll Enterococcus faeca Human OVCA2 tumour Aminopeptidase Ol2 Aminopeptidase Ol2 Human OVCA1 tumour Human OVCA1 tumour	Human secreted pro Breast cancer mamm MMTV env protein n Partial human comp
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119 120 20 20	20 20 20 18	13 13 13 13	750 170 170 170 170	13 20 17 16 17	20 18 21 12
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## ALIGNMENTS

Infection: pathogenic Leptospira; protective immunity; therapy; diagnosis; ss. Leptospira rRNA gene nucleotide sequence. BP. 20-JAN-1999 (first entry) V58901 standard; DNA; 22 Leptospira sp. WO9840099-A1 V58901; RESULT V58901 

98WO-AU00145. 06-MAR-1998; 17-SEP-1998

97AU-0005494. 07-MAR-1997; (AGRI-) AGRIC VICTORIA SERVICES PTY LTD. (PIGR-) PIG RES & DEV CORP.

Chappel RJ;

WPI; 1998-520791/44.

New isolated pathogenic Leptospira bacterium - useful for, e.g developing products for conferring protective immunity, and for prophylactic or therapeutic treatment

Claim 15; Page 72; 94pp; English.

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Infection; pathogenic Leptospira; protective immunity; therapy;
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                                                                                                                                                                                L. fainei nucleotide sequence
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           This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainei. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species
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(PIGR-) PIG RES & DEV CORP.
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New isolated pathogenic Leptospira bacterium - useful for, e.g developing products for conferring protective immunity, and for prophylactic or therapeutic treatment
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XX T90543; DT 13-FEB-1998 (first entry) DE Maize male fertility gene Z33 XX
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetla deficiency; blood; allergy; renal; ds; immune system; asthma lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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97US-0048876.
97US-0048880.
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97US-0048898
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                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This DNA sequence comprises the maize 233 Zm41-A gene. This is an orthologue of Arabidopsis Ms41-A (see 190522), a gene that confers male fertility. It was obtained following a database search for sequences that showed homology to Ms41-A DNA, isolation of a partial cDNA clone, and use of this clone to isolate Zm41-A genes (Z 231 (190542), Z33 (190543) and Z35 (190544) from genomic lambda libraries. The genes show a high level of conservation. Z35 may be derived from Z31 via genetic rearrangements, deletions and/or insertions. Z33 has subsequent deletions from Z35 and is truncated, having only exons 3, 5 and 6. The Ms41-A and Zm41-A genes, antisense or ribozyme sequences can be used to produce transagenic plants with controlled male fertility. Male sterile plants are useful for hybrid seed production, particularly in plants where restoration of fertility is not needed, e.g.
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Zm41-A; male fertility; hybrid seed; transgenic plant; antisense;
ribozyme; male sterile; maize; Ms41-A; ds.
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                                                                                 Location/Qualifiers
823..915
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268 TGTTGAATCACAAGATCTGA 249
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936..1090
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1168..1332
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916..935
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Best Local Similarity
Matches 18; Conserva
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                                                  Zea mays
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us-09-380-826a-2.rng

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V59636;
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CC encoding human secreted proteins (w88534 to w88756). The secreted protein

CG gene sequences are deposited with the ATCC under deposit numbers ATCC

Gene sequences are deposited with the ATCC under deposit numbers ATCC

G1979, 97974, 97976, 97976, 97977, 209007, 209008, 209010,

CC 509011, 209080, 209081, 209083, 209084, 209085, 209511. Host

CC cells comprising recombinant vectors containing the nucleic acid

cells comprising recombinant vectors containing the nucleic acid

CC sequences are used for the recombinant production of the secreted

CC sequences are used for the recombinant orid sequences are useful for are

proteins. The polynucleotide and amino acid sequences are useful for are

CC sequences are used for the new polypeptides in a sample or by

CC determining the presence of mutations in the new polynucleotides, based on

Specific uses are described for each of the polynucleotides, based on

Specific uses are described for each of the polynucleotides, based on

Specific uses are described for each of the polynucleotides, based on

Specific uses are described for each of the polynucleotides, based on

CC disorders, developmental abnormalities and focial deficiencies, blood

cd isorders, tumours, leukemias, diseases of the immune system, autoimmune

cd isorders, tumours, leukemias, diseases of the immune system, altoimmune

cd isorders, prostate diseases, obesity, disorders involving osteoclasts

cr chymus, diseases, sarthritis or malignancies, diseases of testes, lung

cr chymus, diseases, section or malignancies, diseases of testes, lung

cr chymus, diseases, section or malignancies, diseases of testes, lung

cr chymus, diseases, obesity, disorders involving osteoclasts

cr chymus, diseases, section or malignancies, diseases of testes, lung

cr chymus, diseases, section or malignancies, diseases of testes, lung

cr chymus, diseases, described pricine diseases, diseases of testes, and copulity disorders and AlbS. The

CD polypepti
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Fan P, Feng P, Ferrie AM, Fischer CL, Florence C;
Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW;
LI Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM;
Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
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85.7%; Pred. No. 47
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                                        970S-0048963.
970S-0048971.
970S-0049019.
970S-0057627.
970S-0057634.
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P-PSDB; W88721.
06.JUN-1997;
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05-SEP-1997
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemla; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenta; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                          Human secreted protein gene 126 clone HELGH31.
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970S-0047583.
970S-0047584.
970S-0047585.
970S-0047586.
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97US-0047492.
97US-0047500.
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970S-0043569.
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97US-0047503.
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97US-0047598
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97US-0040626.
97US-0043311.
'6/c
V59636 standard; DNA; 1291 BP.
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97US-0040333.
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97US-0043313.
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97US-0040162
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                                           19-JAN-1999 (first entry)
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23-MAY-1997;
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23-MAY-1997,
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Pred. No. 47; ; Mismatches

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Query Match
Best Local Similarity 85.7
Matches 18; Conservative

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Gaps

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209048) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Pc portion (e.g. v59501) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: v95311-v85012; amino acid sequences WA7731-W73056) which are useful for preventing, treating or ameliocating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see V5511 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polyeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in manans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Borrelia burgdorferi nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
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Pred. No. 48;
0; Mismatches
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97US-0050359.
97US-0053344.
97US-0053377.
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85.7%;
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                                                                                                                                                                                                                                             Query Match 73.6
Best Local Similarity 85.7
Matches 18; Conservative
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P-PSDB; Y20060.
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22-JUL-1997;
22-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
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 9705-0047599
9705-0047690
9705-0047613
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Query Match
Best Local Similarity
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Matches 18; Conserv
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Wyse DL;
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                                                             Gaps
                                                                                                                                                                                                                                                           Malze; acetyl-CoA-carboxylase; fluazifop; sethoxydim; herbicide; probe; transcarboxylase active site; biotin binding site; probe; transit peptide; plasmid; screening; cassette; antisense; promoter; transit peptide; plasmid; tissue-specific gene expression; herbicide resistance; oilseed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expression cassette containing plant acetyl CoA gene - used to confer herbicide tolerance or to increase oil content of plants
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/product= Transcarboxylase active site region
59..70
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                                       Length 1473;
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                                                                Indels
     sequence 1473 BP; 622 A; 232 C; 121 G; 498 T; 0 other;
                                                                                                                                                                                                                                                                                                            oil content; transgenic plant; crop improvement; ss
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                                          20;
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/product= Biotin binding site
                                          DB
                                         Score 16.2; 1
Pred. No. 49;
                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Column 35-38; 31pp; English.
                                                                                                                                                                                                                                            Acetyl-CoA-carboxylase gene fragment.
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1770..1946
/*tag= a
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90US-0538674.
92US-0917462.
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                                                                                                                68 GCTGCATCACAGGATTTGATA 48
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                                            Query Match 73.6%;
Best Local Similarity 85.7%;
Matches 18; Conservative
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Wyse DL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      portion of a maize acetyl con carboxylase (ACCase) gene located at portion of a maize acetyl codo carboxylase (ACCase) gene located at bases 2883 to 83 from the 3' stop codon. Clone #15-14 was isolated from a lambda gtil cDWA library of maize inbred A186 seedlings by from a lambda gtil cDWA library of maize inbred A186 seedlings by screening with maize ACCase antiserum. Other ACCase DNA fragments screening with maize ACCase antiserum. ACCase DNA can be incorporated (W05590) have also been isolated. ACCase DNA can be incorporated into a vector and used to increase the herbicide tolerance or oll into a vector and used to increase the herbicide tolerance or oll heterologous systems.
                                                                                                                                                                                                                                                                                                                                               Gaps
promoter, e.g. a cauliflower-mosaic virus 35S promoter or mopaline-synthase promoter, and N-terminal maize chloroplast transit peptide sequence in a plasmid vector for high-level tissue-specific gene expression, to confer herbicide resistance and/or alter the oil content of the plant, or to increase the plant and/or alter the oil content of the plant, or to increase the plant and paid, so that the crystallized enzyme may be used to screen and identify other herbicides that bind to and inhibit the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A 2 kb EcoRI fragment (T39904) of lambda clone #15-14 includes a
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in. of plants with herbicide tolerance or altered oil content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maize acetyl CoA carboxylase cDNA clone EcoRI fragment.
                                                                                                                                                                                                                  Sequence 2000 BP; 546 A; 406 C; 494 G; 554 T; 0 other;
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pred. No. 51;
0; Mismatches
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85.7%; Pred. No. 51;
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85.7%;
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BP.

(first entry)

95FR-0012162. 95FR-0012162.

Fsihi H;

us-09-380-826a-2.rng

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Mycobacterial DNA gyrase precursor protein - and polypeptide(s) corresponding to mycobacterial DNA gyrase intein sequences
                                                                                                                                      Mycobacterium sp.; internal sequence; intein; immature; gyrase; protein splicing; precursor; gyrA; ss.
                                                                                                             M. leprae gyrA precursor coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Pages 33-34; 55pp; French
                                    T64683 standard; DNA; 3822
                                                                                                                                                                            Mycobacterium leprae.
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                                                             T64683;
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             RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA encoding acetyl-CoA carboxylase from oats, used to produce transformed plants with herbicide resistance and altered oil content
                                                                                                                                                             EcoRI fragment of lamda clone #15-14 with maize ACCase gene portion.
                                                                                                                                                                                               maize acetyl CoA carboxylase; AcCase; herbicide; plant oil content; marker-assisted plant:selection; groat oil trait; restriction fragment length polymorphism mapping; high-energy animal feed; low-fat human food; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Somers DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2001;
                                                                                                                                                                                     Herbicide resistance; gene modification; lamda clone #15-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rines HW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       food and in genetic dissection of the groat oil trait.
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Pred. No. 51;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                             US DEPT OF AGRICULTURE.
EGLI M A.
GROH S.
             42 gttggatgacaagagttgtta 62
                                                                                    Z49816 standard; DNA; 2001 BP
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Best Local Similarity 85.7%;
Matches 18; Conservative (
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PHILLIPS R L.
RINES H W.
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02-JUL-1998;
                                                                                                                                                                                                                                                                Zea mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KIAN/) H
(PHIL/) H
(RINE/) H
(SOME/)
                                                                                                                                                                                                                                                                                                                                                                                                               (USDA )
(EGLI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                       (GROH/)
                                                                                                             249816;
                                                             RESULT
Z49816
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This DNA, isolated from Mycobacterium leprae, encodes a precursor (immature) gyrase protein from which an "intein" (see W15074) is excised during maturation. The gyrase and its coding sequence are useful to fabricate products that alter the maturation of proteins essential for the development of infectious agents by altering the protein splicing of precursor polypeptides of the proteins. The inteins encoded by the gyrasenes of Mycobacterium leprae, M. flavescens, M. gordonae and M. kansasii are used: (a) to modify the genome of a eukaryotic call that lacks endogenous biological activity identical to that of the polypeptide; (b) to replace a copy of a gene present in a recipient genome by integration of a gene different from that where the integration takes place; and (c) for targetted insertion of a foreign DNA sequence into a selected site in the genome of a eukaryotic cell not containing the specific cleavage sites of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3822;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3822 BP; 843 A; 899 C; 1092 G; 988 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.2; DE
Pred. No. 54;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2334 gttggatcagatgatttgtta 2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A3 maize ACCase cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q42933 standard; DNA; 4346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 gttggatcacaagatttgata
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Best Local Similarity
Matches 18; Conserv
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Gaps

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Indels

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2 gttggatcacaagatttgata 22 

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902 gttggatgacaagagttgtta 922

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The sequence is that of the A3 acetyl coA carboxylase (ACCase) CDNA maize cloue which can be used to probe plant DNA to isolate other such clones. It may be used with plant regulatory sequences to such clones. It may be used with plant regulatory sequences to requested to assettes for ACCase. These cassettes are used to produce expression cassettes for ACCase. These cassettes are used to composition of seeds or other plant parts, e.g. enabling oil.

CC the composition of seeds or other plant parts, e.g. enabling oil.

CC bearing plants such as oilseed rape, sunflower or oilpalm, having a lower or modified oil content to be produced. It can be used to form lower or modified oil content to be produced. It can be used to form cassettes for overexpression of ACCase., leading to produ. CC of plants with an increased oil content. It may also be used to recover the ACCase expression of moncotyledonous plants can be made to inhibit ACCase expression. Moncotyledonous plants can be made consistent to grass-weed herbicides such as fluazifop and alkylketones resistant to grassion of moncot ACCase, expression of dict acheived by overexpression of moncot ACCase, expression of dict content to these herbicides. This is content which weeds growing between the plants. This allows the overall destroy weeds growing between the plants. This allows the overall destroy weeds growing the method, weeds such as wild oats may be previous crop. Using the method, weeds such as wild oats may be previous crop. Using the method, weeds such as wild oats may be previous error and the farmer is given extra options to obtain an improved controlled, and the farmer is given extra options to more effective.
Acetyl coA carboxylase; ACCase; probe; expression; oil content; lower; modified; increased; oilseed rape; sunflower; resistant; resistance; grass-weed herbicides; fluazifop; alkylketones; maize; wheat; barley; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          query Match 73.6%; Score 16.2; DB 14; Length 4346; Best Local Similarity 85.7%; Pred. No. 55; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA clones for use in probing plant DNA - comprise maize acetyl coenzyme-A carboxylase gene flanked by heterologous DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4346 BP; 1239 A; 829 C; 1064 G; 1213 T; 1 other;
                                                                                                                                                                                                                                                       /*tag= b
/note= "GAN encodes Glu or Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suitable crops are maize, wheat and barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ICIL ) ICI AUSTRALIA OPERATIONS PTY LTD. (ICIL ) IMPERIAL CHEM IND PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitfeld PR;
                                                                                                                                                  Location/Qualifiers
3.3947
/*tag a
/note= "AcCase"
1875.1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 3; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           92WO-GB02205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ashton AR, Jenkins CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-197061/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; R36781.
                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-1991;
                                                                                                                                                                                                                                                                                                                  WO9311243-A.
                                                                                                                                                                                                                                                                                                                                                        10-JUN-1993.
                                                                                                                       Zea mays.
                                                                                                                                                               Key
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A CDNA sequence (T39905) codes for maize acetyl COA carboxylase (ACCase) (W05590), an enzyme that plays a central role in fatty acid biosynthesis and accumulation in plants and seeds. The complete sequence was deduced from CDNA clone #18-5, obto. from a lambda gtll cDNA library of maize inbred A188 seedlings, and from PCR amplifications (see also T39918-23). Genomic ACCase DNA fragaments have also been isolated (see also T39906-16). ACCase DNA regaments have also been isolated (see also T39906-16). Accase DNA herbicide tolerance or oil content of a transgenic plant, or used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding maize acetyl coenzyme A carboxylase gene · used for prodn. of plants with herbicide tolerance or altered oil content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7470;
                                                                                                                 Acetyl COA carboxylase; ACCase; herbicide tolerance;
cyclohexanedione; aryloxyphenoxypropionic acid; vegetable oil;
oilseed; maize; corn; SS.
                                                                                                                                                                                                                                                                                                                                                                                            Somers DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7470 BP; 2119 A; 1429 C; 1844 G; 2071 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                             Gronwald JW, Lutz SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 58;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.6%; Score 16.2; I
85.7%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to produce ACCase in heterologous systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 78-80; 131pp; English.
                                                                                                                                                                                                 Location/Qualifiers
37..7014
/*tag= a
                                                                                                                                                                                                                                        /EC_number= 6.4.1.2
                                                                                               Maize acetyl CoA carboxylase cDNA.
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                    T39905 standard; cDNA; 7470 BP
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                         23-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Gengenbach BG,
                                                                                                                                                                                                                                                                                                                                                                      (MINU ) UNIV MINNESOTA
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                                                                                                                                                                             Zea mays line A188.
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                                                                                                                                                                                                                                                                     WO9631609-A2
                                                                                                                                                                                                                                                                                                                       04-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Wyse DL;
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                                                   T39905;
RESULT 13
T39905
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us-09-380-826a-2.rng

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maize acetyl CoA carboxylase; ACCase; herbicide; plant oll content; marker-assisted plant selection; groat oll trait; restriction fragment length polymorphism mapping; high-energy animal feed; low-fat human food; ss.
                                                                     Herbicide resistance; gene modification;
                                              Maize acetyl CoA carboxylase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Egli MA, Groh S, Kianian SF,
                      18-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-147205/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; Y44687
                                                                                                                                                                                                                                                                              W09967367-A1
                                                                                                                                                                                                                                                                                                                             22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                   22-JUN-1998;
02-JUL-1998;
                                                                                                                                                                                                                                                                                                      29-DEC-1999
                                                                                                                                            Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                         (GROH/) (KIAN/) (PHIL/) (RINE/) (SOME/)
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249820;
                                                                                                                                                                                                                                                                                                                                                                                                   (USDA)
                                                                                                                                                                                                                                                                                                                                                                                                                EGLI/)
                                                                                                                                                                                                                                            3'UTR
                                                                                                                                                                                                                    5'UTR
                                                                                                                                                                    Key
This cDNA encodes a maize ACCase enzyme. This can be used in a method of preparing an herbicide resistant corn plant which comprises crossing a first corn plant to a second corn plant so as to yield a progeny plant, where the first corn plant comprises at least 1 herbicide resistant allele and the second plant comprises at least 1 herbicide resistant allele which is not allelic to the herbicide resistant allele present in the first plant. The herbicide resistant corn plants are prepared using Acc1 and Acc2 gene combinations which impart cylcohexanedione (CHD) or aryloxyphenoxypropanoic acid (APA) herbicide tolerance to the corn plants. The methods are used to impart cillo and APA herbicide tolerance to corn plants and to produce CHD or APA herbicide tolerant Zea mays (Corn) homozygous or heterozygous for Acc1 and homozygous or heterozygous for Acc1 and homozygous or heterozygous for Acc2. The methods can also be used to impart tolerance to a corn plant to an agent which inhibits acetyl COA carboxylase, selected from 3.(2.4-dichlorophenyl)-perhydroludolizine-2,4-dione, 3-isopropyl-6.
                                                          corn plant; tolerance; Acc1; Acc2;
                                                       ACCase; maize; herbicide resistant; corn plant; tolerance; Accl; Acc2 cylcohexanedione; CHD; aryloxyphenoxypropanolc acid; APA; enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                            Herbicide resistant corn plants - prepared using Acc1 and Acc2 gene combinations
                                                                                                                                                                                                                                                                                                                                        Marshall LC, Parker WB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7470 BP; 2119 A; 1429 C; 1844 G; 2071 T; 7 other;
                                                                                                                                                                 Ser)
                                                                                                                                                        His)
                                                                                                                                                                 aa:
                                                                                                                                                          aa:
                                                                                                                                        /*tag= a //transl_except= (pos:4339..4341, //transl_except= (pos:4456..4458, //transl_except= (pos:4359..4461, /product= "AcCase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      soraphen A and their structural analogues.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Fig 3A-E; 112pp; English.
                                                                                                                                                                                                                                                                                                                                        SM,
                                                                                                                  Location/Qualifiers
37..7014
/*tag= a
                                   Maize ACCase enzyme encoding cDNA
                                                                                                                                                                                                                                                                                                                                         , Lutz SN
Wyse DL;
                                                                                                                                                                                                                                                                                          96US-0697826
           (first entry)
                                                                                                                                                                                                                                                                                                                                        Gengenbach BG,
                                                                                                                                                                                                                                                                                                                                                   Vandee KL,
                                                                                                                                                                                                                                                                                                                (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-207043/18.
P-PSDB; W56736.
                                                                                                                                                                                                                 WO9808963-A1
                                                                                                                                                                                                                                                                 29-AUG-1997;
                                                                                                                                                                                                                                                                                         30-AUG-1996;
           30-JUL-1998
                                                                                                                                                                                                                                         05-MAR-1998
                                                                                                                                                                                                                                                                                                                                                     Somers DA,
                                                                                              Zea mays.
                                                                                                                                                                                                                                                                                                                                        Egli MA,
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/product= "Maize acetyl CoA carboxylase"

/\*tag= b 7014..7470

/\*tag= c

Location/Qualifiers 37..7014

/\*tag= a

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                                                                                                                                                                                Accase is involved in fatty acid synthesis and is the target of the specified herbicides. Transformation of plants with Accase imparts resistance to cyclohexamedione and aryloxyphenoxypropanolc acid herbicides and alter the oil content. The Accase DNA is also used as source of probes and primers for the identification of transgenic plants; in marker-assisted plant selection and for restriction fragment length polymorphism mapping, used for high-energy animal feed and high-fiber, low-fat human food and in genetic dissection of the groat
                                                                                                                                                             The present cDNA sequence encodes maize acetyl COA carboxylase (ACCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
New DNA encoding acetyl-CoA carboxylase from oats, used to produce transformed plants with herbicide resistance and altered oil content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.6%; Score 16.2; D
85.7%; Pred. No. 58;
iive 0; Mismatches
                                                                                             Example 6; Fig 13; 197pp; English.
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             oil trait
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73.6%; Score 16.2; D 85.7%; Pred. No. 58; iive 0; Mismatches

Query Match
Best Local Similarity 85.7
Matches 18; Conservative

3972 gttggatgacaagagttgtta 3992

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gttggatcacaagatttgata

Z49820 standard; cDNA; 7470 BP

RESULT 15 249820 ID 24 XX

DB 19; Length 7470;

Somers DA;

Rines HW,

Phillips RL,

UNIV MINNESOTA. US DEPT OF AGRICULTURE. EGLI M A.

PHILLIPS R L.

KIANIAN S F. RINES H W. SOMERS D A

99WO-US14022. 98US-0090240. 98US-0091640.

Search completed: March 27, 2001, 08:22:58 Job time: 5300 sec

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USA
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Sequence 5, Appli
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26.799 Million cell updates/sec
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Sequence 1, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4,
Sequence 3,
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                                                                                                                                                                                                                                                               March 27, 2001, 08:19:18; Search time 132.3 Seconds
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-399-986B-3
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US-08-399-986B-1
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Match Length DB · ID
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
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Sequence 68, Appl	PCT-US94-02891-68	₹ (	1608	66.4	14.6	44	O
Sequence 1, Appli	US-08-424-224-1	~	1608	66.4	14.6	43	O
Sequence 4, Appli	US-08-467-831-4	~	1404	66.4	14.6	42	
Sequence 3, Appli	US-08-467-831-3	7	1404	66.4	14.6	41	
Sequence 2, Appli	US-08-467-831-2	Н	1404	66.4	14.6	40	
Sequence 1, Appli	US-08-467-831-1	Н	1404	66.4	14.6	39	
Sequence 4, Appli	US-08-470-702-4	Н	1404	66.4	14.6	38	
ω,	US-08-470-702-3	-	1404	66.4	14.6	37	
7	US-08-470-702-2	-	1404	66.4	14.6	36	
-	US-08-470-702-1	٦	1404	66.4	14.6	35	
7	US-08-204-656B-7	Н	1404	66.4	14.6	34	
'n	US-08-204-656B-5	-1	1404	66.4	14.6	33	
m	US-08-204-656B-3	~	1404	66.4	14.6	32	
Sequence 1, Appli	US-08-204-656B-1	Н	1.404	66.4	14.6	31	
Sequence 13, Appl	US-08-866-340-13	m	293	66.4	14.6	30	
Sequence 1, Appli	US-08-880-179-1	٣	9919	67.3	14.8	29	

## ALIGNMENTS

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RESULT 1

US-08-014-326-1

Sequence 1, Application US/08014326

Patent No. 5498544

GENERAL INFORMATION:

APPLICANT: Gengenbach, Burle G.

APPLICANT: Growald, John W.

APPLICANT: Growald, John W.

APPLICANT: Bali, Margaret A.

APPLICANT: Bali, Margaret A.

APPLICANT: Bali, Margaret A.

APPLICANT: Bali, Margaret A.

APPLICANT: Hinneapolis S.

CORRESPONDER: Marchant & Gould

STREET: 3100 No. 5498544west Center

CITY: Minneapolis S.

COMPUTER: TBM PC compatible

PELICATION NUMBER: US 07/917,462

FILING DATE: 21-UL-1992

CLASSIFICATION NUMBER: US 07/538,674

FILING DATE: 21-UL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/269,584

FILING DATE: 11-UL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/269,584

FILING DATE: 31-UN-1990

REGISTRATION NUMBER: 36,988

FILING DATE: 31-UN-1990

TELEPHONE: 612-332-9081

INFORMATION FOR EQUID NO: 1:

SECOUNDER: 210-NOV-1988

RESISTRATION NUMBER: 36,988

RESISTRAT
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                 METHODS AND AN ACETYL COA CARBOXYLASE GENE
FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN
OIL CONTENT OF PLANTS
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                                                                                                                         Length 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Somers, D. A.
APPLICANT: Wyse, D. L.
APPLICANT: Gronwald, J. W.
APPLICANT: Gronwald, J. W.
APPLICANT: Gronwald, J. W.
APPLICANT: Lutz, S. M.
TITLE OF INVENTION: METHOD FOR PRODUCING PLANT ACETYL COA
CORRESPONDENCES: 11
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O. Box 2938 CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2001 Dase pairs
TYPE: nucleic acid
TYPE: single
                                                                                                                           DB 1;
                            : IMMEDIATE SOURCE: ; CLONE: 2 kb fragment of lambda clone #15-14 US-08-014-326-1
                                                                                                                        Score 16.2; Di
Pred. No. 20;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.6%; Score 16.2; D
85.7%; Pred. No. 20;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                           US-08-417-089-1

Sequence 1, Application US/08417089

Patent No. 6069298

GENERAL INFORMATION:

APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/08695651; Patent No. 6146867; GENERAL INFORMATION:
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linear
E: DNA (genomic)
                                                                                                                                                                                            2 gttggatcacaagatttgata 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gengenbach, B. G.
                                                                                                                        73.6%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METH
TITLE OF INVENTION: FOR
TITLE OF INVENTION: OIL
NUMBER OF SEQUENCE: 11
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 73.6
Best Local Similarity 85.7
Matches 18; Conservative
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COMPUTER READABLE FORM:
                                                                                                                      Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
 TOPOLOGY: 11
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APPLICANT:
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US-08-695-651-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ASHTON, ANTHONY R.
APPLICANT: JENKINS, COLIN L.D.
APPLICANT: WHITFELD, PAUL D.
TITLE OF INVENTION: MAIZE ACETYL COA CARBOXYLASE ENCODING
TITLE OF INVENTION: DNA CLONES
TITLE OF EQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,537
FILING DATE: US-08/244,537
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
T: 1100 New York Avenue, N.W.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.6%; Score 16.2; 1
Best Local Similarity 85.7%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 600.318US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
                                                                                   FILING DATE: 12-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/417089
FILING DATE: 05-APR-1995
APPLICATION NUMBER: 08/014326
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 07/917462
FILING DATE: 1-JUL-1992
APPLICATION NUMBER: 07/538674
FILING DATE: 18-JUN-1990
ATTOMNEY/AGENT INFORMATION:
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/695,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08244537 Patent No. 5854420 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 gttggatcacaagatttgata 22
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                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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GB 9125330.2

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APPLICANT: Goltry, Kristin L.
APPLICANT: Greenberger, Joel S.
TITLE OF INVENTION: DETERMINING EXPOSURE TO IONIZING RADIATION
TITLE OF INVENTION: AGENT WITH PERSISTENT BIOLOGICAL MARKERS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7470;
            APPLICANT: Myse, D. L.
APPLICANT: Gronwald, J. W.
APPLICANT: Egli, M. A.
APPLICANT: LULE, S. M.
APPLICANT: LULE, S. M.
TITLE OF INVENTION: METHOD FOR PRODUCING PLANT ACETYL COANUMBER OF SEQUENCES: 11
                                                                                                                                                E: Schwegman, Lundberg, Woessner & Kluth, P.A.
P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/695,651
FILING DATE: 12-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/417089
FILLING DATE: 05-APR-1995
APPLICATION NUMBER: 08/014326
FILLING DATE: 05-FEB-1993
APPLICATION NUMBER: 07/917462
FILING DATE: 21-JUL-1992
APPLICATION NUMBER: 07/538674
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-602-145-14/c
; Sequence 14, Application US/08602145
; Patent No. 6025336
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3972 GTTGGATGACAAGAGTTGTTA 3992
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,4
                                                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 7470 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 85.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             Minneapolis
                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
SOFTWARE: FastSEC
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                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                        55402
                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                        COMPUTER:
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FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN
OIL CONTENT OF PLANTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
PRIOR PAPLICATION DATA:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02205
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 203094/SEE 36663/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEPA: 6714627 CUSH
TELEPA: 6714627 CUSH
TELEPA: 6714627 CUSH
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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85.7%; Pred. No. 23;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                             73.6%; Score 16.2;
85.7%; Pred. No. 22;
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7470 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
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Patent No. 6146867
GENERAL INFORMATION:
APPLICANT: Gengenbach, B. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3972 GTTGGATGACAAGAGTTGTTA 3992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         902 GTTGGATGACAAGAGTTGTTA 922
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic) US-08-417-089-5
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.0°
Best Local Similarity 85.7°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.6 Best Local Similarity 85.7 Matches 18; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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US-08-417-089-5
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DB 1; Length 1096;
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COTHER INFORMATION: the coding region shown in (2)(ix)(B)
CHER INFORMATION: codes for the protein of SEQ ID NO: 3
US-08-684-862-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rollin, Pierre E.
APPLICANT: Elliott, Luanne
APPLICANT: Kaiazek, Thomas G.
APPLICANT: Morzunov, Sergey
APPLICANT: Morzunov, Sergey
APPLICANT: Ravkov, Eugeny
TITLE OF INVENTION: The Black Creek Canal Hantavirus and
TITLE OF INVENTION: Related Methods
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION 'DATA:
APPLICATION NUMBER: US/08/792,055
FILING DATE: 03-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: NEEDLE & ROSENBERG, P.C.
127 Peachtree Street, N.E., Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    70.9%; Score 15.6; 1
81.8%; Pred. No. 37;
                                                                                                                           MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Agkistrodon rhodostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/390,361
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414
TELECOMMUNICATION INFORMATION:
TELEFAN: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08792055
Patent No. 5853980,
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 tgttggatcacaagatttgata 22
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             SEQUENCE CHARACTERISTICS:
LENGTH: 1096 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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MEDIUM TYPE: Floppy
                                                                                                           linear
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STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-792-055-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-792-055-1
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Patent No. 5759541
GENERAL INFORMATION:
APPLICANT: Bach, Alfred
APPLICANT: Bialojan, Siegfried
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 14
CORRESOUNDENCE ADDRESS:
ADDRESSEE: Kell & Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                   COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,145
FILING DATE: 15-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Beach, Stephen A:
REGISTRATION NUMBER: 29,768
FREISCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5309
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM AT-COMPATIBLE, 80286 processor OPERATING SYSTEM: MS-DOS version 5.0 SOFTWARE: WordPerfect version 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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81.8%; Pred. No. 31
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,040
FILING DATE: 30-DEC-1992
APPLICATION NUMBER: PCT/EF91/01361
FILING DATE: 19-JUL-1991
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APPLICATION NUMBER: US/08/361,705
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 TTTTGCATCATAACATTTGATA 267
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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US-08-602-145-14
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Best Local Similarity 81.8
Matches 18; Conservative
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         COUNTRY: USA
ZIP: 20007-5109
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Sequence 1, Application US/08874162
Patent No. 5872216
GENERAL INFORMATION:
APPLICANT: Hannah, L. Curtis
APPLICANT: Giroux, Michael
TITLE OF INVENTION: Materials and Methods for Increasing
TITLE OF INVENTION: Corn Seed Weight
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                 ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ed. No. 46;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.6;
                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/299,675
FILING DATE: 1-SEP-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REERSNEC/DOCKET NUMBER: UF146.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/874,162 FILING DATE: 13-JUN-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/485,241
                                                                                                                                                                                                     PC-DOS/MS-DOS
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                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 7745 base pairs
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Best Local Similarity 81.8
Matches 18; Conservative
                                                                                           COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY di
COMPUTER: IBM PC COMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS
                                  STREET: 2421 N.M. CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gainesville
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                                    Length 1989;
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Sequence 1, Application US/08485241
Sequence 1, Application US/08485241
GENERAL INFORMATION:
APPLICANT: Hannah, L. Curtis
APPLICANT: Giroux, Michael
TITLE OF INVENTION: Materials and Methods for Increasing
TITLE OF INVENTION: Corn Seed Weight
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                  Sequence 1, Application US/08299675
Patent No. 5589618
GENERAL INFORMATION:
APPLICANT: Hannah L. Curtis
APPLICANT: GLIOUX, Michael
TITLE OF INVENTION: Materials and Methods for Increasing
MINDER OF ENVIRON: Corn Seed Weight
                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-50S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,675
                                                                            4;
                                    DB 2;
                   70.9%; Scur.
81.8%; Pred. No. 3>,
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.9%; Score 15.6;
81.8%; Pred. No. 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794 REFERENCE/DOCKET NUMBER: UF146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3600 TGTTGGATAACAAGATGACATA 3579
                                                                                                                                        . 288 TGTTGGATCAACAGATTTTGTA 267
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                                                                                                                1 tgttggatcacaagatttgata 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 7745 base pairs
                                                                          18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            904-372-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 18; Conserva
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                                    Query Match
Best Local Similarity
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STATE: FL
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US-08-299-675-1/C
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Gaps

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Length 7745;

DB 1; Length 1016;

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Query Match
Best Local Similarity 85.01
Matches 17; Conservative
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: Godwin,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19103-2307
           US-08-399-9868-3
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Sequence 3, Application US/08399986B

Patent No. 58010101

GENERAL INFORMATION:
APPLICANT: Godwin, Andrew K.
TITLE OF INVENTION: No. 5801041el Gene Associated with Suppression TITLE OF INVENTION: Tumor Development
NUMBER OF SEQUENCE: 35
CORRESPONDES: 35
CORRESPONDES: 1601 Market Street
STREET: 1601 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 7745;
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ZIP: 19103-2307

COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION DATA: US/08/399,986B
FLING DATE: 06-MAR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.9%; Score 15.6; D
81.8%; Pred. No. 46;
tive 0; Mismatches
                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
TLUNG DATE: 1-5EP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PACE, DOTAIN R. 38,261
REGISTRATION NUMBER: 38,261
TELEPHONE: 352-375-8100
TELEPAX: 352-375-8100
APPLICATION NUMBER: US 08/485,241
FILING DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3600 TGTTGGATAACAAGATGACATA 3579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION UNDMER: 27,643
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1016 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 tgttggatcacaagatttgata 22
                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-874-162-1
                                                                                                                                                                                                                                           TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7745 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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EDNESS: double
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No. 5821338el Gene Associated with Suppression
of Tumor Development
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No. 5801041el Gene Associated with Suppression
of Tumor Development
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                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/493,754A FILING DATE: 22-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street
CITY: Philadelphia
69.1%; Score 15.2; 1
85.0%; Pred. No. 57;
                                                Mismatches
                                                                                                                                                                                   RESULT 14
US-08-493-754A-3/C
US-08-493-754A-3/C
Sequence 3, Application US/08493754A
Patent No. 5821338
GENERAL INFORMATION: Andrew K.
APPLICANT: GODAIN, AND S821338E1 G
TITLE OF INVENTION: Of TUMOr Develc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-399-986B-1/C
; Sequence 1, Application US/08399986B
; Patent No. 5801041
                                           ;
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NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
TELECOMMUNICATION INFORMATION:
                                                                                                         830 TTGGGTCTCAAGAATTGATA 811
                                                                              3 ttggatcacaagatttgata 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                830 TTGGGTCTCAAGAATTGATA 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (215) 563-4100
TELEFRAX: (215) 563-4044
INFORNATION FOR SEO ID NO. 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1016 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ttggatcacaagatttgata
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                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street
CITY: Philadelphia
STRET: 1601 Market Street
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
ZIP: 19103-2307
COMPUTER: Labor Compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/OM/399,986B
FILING DATE: 06-MR-1995
CLASSIFICATION NUMBER: US/OM/399,986B
FILING DATE: 06-MR-1995
CLASSIFICATION INFORMATION:
TELEPAN: (215) 563-4004
INFORMATION FOR ED IN OO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2125 base pairs
TOPOLOGY: NOO FERVANCE
HYPOFIE TO COM CHEVANCE
HYPOFIETICAL: NO
ANTI-SENSE: NO
WANTI-SENSE: NO
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Gaps

Search completed: March 27, 2001, 08:19:19 Job time: 5146 sec

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linear
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20004-1008
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Best Local Similarity
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US-08-631-751A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
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Sequence 1329, Ap.
Sequence 1729, Ap.
Sequence 1731, Ap.
The sequence 1732, Ap.
The sequence 1732, Ap.
                                                                                    March 27, 2001, 08:19:19; Search time 132.3 Seconds (without alignments) 8.527 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
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Sequence 1
Sequence 1
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Sequence
Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-363-240A-614
US-08-363-240A-615
US-08-374-306A-201
US-08-774-306A-246
US-08-585-684B-1365
US-08-585-684B-1730
US-08-585-684B-1730
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US-08-585-684B-1769
US-08-585-684B-1770
US-08-585-684B-2139
                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -08-166-664-15
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                                                                                                                                                                                                                                                                  280836 segs, 80580151 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             nucleic search, using sw model
                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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7
1 tgttgga 7
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length: 2000000000
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Match Length
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                                                                                                                                                                                                                      Scoring table:
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Maximum DB
                                                             OM nucleic
                                                                                                                                                                                         Sednence:
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                                                                                            Run on:
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## ALIGNMEN

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Microfabricated, Flowthrough Porous
Apparatus for Discrete Detection of Binding Reactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631,751A
FILING DATE: 11-April-1996
CLASSIFICATION: 435
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5.1e+03;
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                                                                                                                                                                           ADDRESSEE: Vinson & Elkins
STREET: 1455 Pennsylvania Avenue, N.W.
Sequence 13, Application US/08631751A

Patent No. 5843767

GENERAL INFORMATION:

APPLICANT: Beattie, Kenneth L.

TITLE OF INVENTION: Microfabricate

TITLE OF INVENTION: Apparatus for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/CDCKET NUMBER: HARCY
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)639-6500
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202)639-6604
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 10 base pairs
                                                                                                                                NUMBER OF SEQUENCES: Î
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                      Washington
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Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.2e+03;
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Patent No. 5610054
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: URHUBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 7; DB 3; 100.0%; Pred. No. 5.2e+(
                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                 FILING DATE: 23-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: SERUNIAN, LESLIE
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 1452-4005
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHRACATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other nucleic acid /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: MALL TOTAL CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/182,968A FTITHG DATE: 13-JANUARY-1994
                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/765,340 FILING DATE: 23-DEC-1996
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 100.v
And 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
  NEW YORK
: NEW YORK
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 TGTTGGA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 tgttgga 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-182-968A-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-765-340-154
                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
               Sequence 19, Application US/08303004
Patent No. 5556955
GENERAL INFORMATION:
APPLICANT: Vergnaud, Gilles
TITLE OF INVENTION: Process for Detection of New Polymor-
TITLE OF INVENTION: phic Loci in an ADN Sequence, Nucleotide Sequences Forming
TITLE OF INVENTION: Hybridisation Probes and Their Biological Applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A
ZIP: 22320
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-FOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/931,311B
FILING DATE: 19920818
ATTORNEY ARGENT INFORMATION:
NAME: Beridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
TELEPANONE; (703) 836-6400
; TELEPANONE: (703) 836-6400
; TELEPANONE: (703) 836-6400
; TELEPANONE: (703) 836-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 7; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: MORGAN & FINNEGAN, L.L.P. 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 154, Application US/08765340 Patent No. 6150092 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                             E: Oliff & Berridge
P.O. Box 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: UCHIDA, K.,
APPLICANT: UCHIDA, T.,
APPLICANT: TANAKA, Y.,
APPLICANT: MATSUDA, Y.,
APPLICANT: KONDO, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: 01iff & B
                                                                                                                                                                                                                                                     CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inear
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US-08-303-004-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 TGTTGGA 6
US-08-303-004-19/c
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US-08-765-340-154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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Gaps
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                                                                                                         Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: COLUME, Larry
APPLICANT: COLUME, James
APPLICANT: Bisgaler, Charles
APPLICANT: Bisgaler, Charles
APPLICANT: Bisgaler, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 7; DB 1; Lv Best Local Similarity 100.0%; Pred. No. 5.2e+03; Matches 7; Conservative 0; Mismatches 0;
                                                                                                      Query Match
100.0%; Score 7; DB 1; L.
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 614, Application US/08363240A
Patent No. 5705388
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 210/(
TELECOMMUNICATION INFORMATION:
TELEPRAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 614:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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13 TGTTGGA 7
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            US-08-182-968A-246
                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEWSULT 5

US-08-182-968A-246/C

Sequence 246, Application US/08182968A

Patent No. 5610054

TOTAL INFORMATION:

APPLICANT: Draper, Kenneth G.

TITLE OF INVENTION: INHIBITING HEPATITIS C.

TITLE OF INVENTION: VIRUS REPLICATION

NUMBER OF SEQUENCES: 497

CORRESPONDENCE ADDRESS:

ADDRESSE:

ADDRESS
PRIOR APPLICATION DATA:
APPLICATION UNDER:
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: WATBURY, Richard 3, 327
REFERENCE/DOCKET NUMBER: 205/277
REFERENCE/DOCKET NUMBER: 205/277
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 246
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|::|||
5 UGUUGGA 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-182-968A-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
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Length 15;
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Patent No. 5869253
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INHIBITING HEPATITIS C TITLE OF INVENTION: UNING REPLICATION NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon 6 Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 7; DB 1; 100.0%; Pred. No. 5.2e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: BM Compatible
OPERATING SYSTEM: BM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363, 240A
FILING DATE: December 23, 1994
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/774,306A FILLING DATE: December 26, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 61
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Los Angeles
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 tgttgga 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: ]
US-08-363-240A-616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                          APPLICANT: COULURE, Larry
APPLICANT: COLLURE, Larry
APPLICANT: Bisgaler, Charles
TITLE OF INVENTION: METHOD AND REGENESSION
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PREVENTION, INHIBITION OF
PROGRESSION AND REGRESSION
OF VASCULAR DISEASES
1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHOD AND REAGENT FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WOR'D PEFFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 616, Application US/08363240A
Patent No. 5705388
GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Pasgaier, Charles
APPLICANT: Page, Michael
TITLE OF INVENTION: METHOD AND REAGEN
TITLE OF INVENTION: PROFENTION, INHIB
TITLE OF INVENTION: PROFESSION AND R
TITLE OF INVENTION: OF VASCULAR DISEAN
NUMBER OF SEQUENCES: 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/363,240A FILING DATE: December 23, 1994 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                Sequence 615, Application US/08363240A
Patent No. 5705388
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440.
TELEX: (7.3510
INFORMATION FOR SEQ ID NO: 615
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Warburg, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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|15 TGTTGGA 9
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US-08-363-240A-616/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: ]
US-08-363-240A-615
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Gaps
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                                                                                                                                                                                                                                                   Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INTORNATION:

APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Jarvis, Thale

APPLICANT: McSwiggen, James

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES

NUMBER OF SEQUENCES: 2751

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 631 West Fifth Street
                                                                                                                                                                                                                                             100.0%; Score 7; DB 2; Lv
100.0%; Pred. No. 5.2e+03;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 35." Diskette, 1.44 Mb
MEDIUM TYPE: 35." Diskette, 1.44 Mb
MEDIUM TYPE: 35." Diskette, 1.44 Mb
MEDIUM TYPE: 50." DISKETTE, 1.00
COMPUTER: IBM Compatible
COMPUTER: IBM P.C. DOS 5.0
SOFTWARE: FastSED Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1366, Application US/08585684B
; Patent No. 5877021
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1366:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                     Conservative
                                                                         TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
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STATE: California
COUNTRY: U.S.A.
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Best Local Similarity
Matches 7; Conserv
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US-08-774-306A-246
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Pred. No. 5.2e+03;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD METHOD METHOD
TITLE OF INVENTION: INHIBITING HEBATITIS C
TITLE OF INVENTION: URBS REPLICATION
NUMBER OF SEQUENCES:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
STREET: 3.01te 4700
CITY: Los Angeles
STREET: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPPRATING SYSTEM: IBM Compatible
OPPRATING SYSTEM: BOOG PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,306A
FILING DATE: December 26, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,968
FILING DATE: May 14, 1992
ATTORNEY AGENT INFORMATION:
ANDEL CATHER MAY 14, 1992
ATTORNEY AGENT INFORMATION:
ANDEL CATHER MAY 14, 1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY,AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
FELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEPAX: (213) 955-0440
TELEPAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELECAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 246, Application US/08774306A
Patent No. 5869253
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TELEPHONE: (213) '489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 246:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 57.1%;
Matches 4; Conservative 3
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US-08-774-306A-246/c
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Sequence 1730, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                       CAPPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: July 7, 1995
ATORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION UNMBER: 32,327
FEFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 1729:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASISEQ Version 1.5
CURREMY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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STATE: California
COUNTRY: U.S.A.
                                         CITY: Los Angeles
STATE: California
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                                                                                         U.S.A.
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US-08-585-684B-1729
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                                                                                         COUNTRY:
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                                                       Sequence 1367, Application US/08585684B

Patent No. 5877021

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: ATAINS, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: MCSA199en, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTY COUNTY COUNTY COUNTY COUNTY COUNTY COUNTY CONDUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: Storage COMPUTER: ENGRAGE COMPUTER: IN COMPATION COMPUTER COURTING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FRASEQ VERSION 1.5 CURRENT APPLICATION DATA:
FILLING DATE: January 16, 1996
PRIOR APPLICATION DATA:
PRILING DATE: JULY 7, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1729, Application US/08585684B Patent No. 5877021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/07
TELECOMMUNICATION INFORMATION:
TELEFAN: (213) 489-1600
TELEFAX: (713) 955-0440
TELEFAX: (731) 955-0440
INFORMATION FOR SEQ ID NO: 1367:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-585-684B-1729/C
                                                US-08-585-684B-1367/c
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APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
TITLE OF INVENTION: MCTHOD AND REAGENT FOR THE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 7; DB 2; L. Best Local Similarity 100.0%; Pred. No. 5.2e+03; Matches 7; Conservative 0; Mismatches 0;
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ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 00/000,951
FILING DATE: JULY 7, 1995
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 31,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 189-1600
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1731:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
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Sequence 1731, Application US/08585684B

; Patent No. 5877021

; GENERAL INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, RICHARD
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEPRA: 67-3310
INFORMATION FOR SEQ ID NO: 1730:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGLE
                                                                                                                                                 218/078
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STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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US-08-585-684B-1730
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-585-6848-1731

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tgttgga 7
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| Db 13 TGTTCGA 7

Search completed: March 27, 2001, 08:19:22
Job time: 5149 sec
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RSV IC hammerhead r
RSV N hammerhead r
RSV N hammerhead r
RSV N hammerhead r
Mouse relA hammerh
Mouse relA hammerh
Human CD40 hammerh
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13 7 100.0 15 16 T56964 RSV 1C ham C 14 7 100.0 15 16 T56964 RSV N hammore 15 100.0 15 16 T57424 RSV N hammore 15 100.0 15 16 T57425 RSV N hammore 16 7 100.0 15 16 T54843 Mouse relA 17 7 100.0 15 16 T54845 Mouse relA 18 7 100.0 15 16 T54841 Human CD40 C 20 7 100.0 15 17 X66632 Human CD40 C 21 7 100.0 15 17 X66633 Human CD40 C 23 7 100.0 15 17 X66635 Human CD40 C 23 7 100.0 15 17 X66826 Mouse CD40 C 24 7 100.0 15 17 X66826 Mouse CD40 C 25 7 100.0 15 17 X66826 Mouse CD40 C 25 7 100.0 15 17 X66826 Mouse CD40 C 25 7 100.0 15 17 X66826 Mouse CD40 C 25 7 100.0 15 17 X66827 Mouse CD40 C 25 7 100.0 15 17 X66827 Mouse CD40 C 25 7 100.0 15 17 X66827 Mouse CD40 C 25 7 100.0 15 17 X66827 Mouse CD40 C 25 7 100.0 15 17 X66827 Mouse CD40 C 25 7 100.0 15 17 X66827 Human B7-1	7 100.0 15 17 X64622 7 100.0 15 18 X75694 7 100.0 15 20 X31695 7 100.0 15 20 X31695 7 100.0 15 21 297690 7 100.0 15 21 297727	36 7 100.0 16 12 011395 37 7 100.0 16 14 052019 Brobe 38 7 100.0 16 16 074138 Basic 39 7 100.0 16 21 297686 HIV-1 40 7 100.0 16 21 297687 HIV-1 41 7 100.0 16 21 297689	7 100.0 16 21 297089 7 100.0 16 21 297702 7 100.0 16 21 297702 7 100.0 16 21 297704 7 100.0 16 21 297702 7 100.0 16 21 297722  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  O-JAN-1999 (first entry)  eptospira nucleotide sequence.  nfection; pathogenic Leptospira; protective immunity; lagnosis; ss.  petospira sp.  O-SEP-1999 (first entry)  FORMAR-1998; 98WO-AU00145.  T-SEP-1998; 98WO-AU00145.  PIGR-) PIG RES & DEV CORP.  PIGR-) PIG RES & DEV CORP.  PI 1998-520791/44.  Ew isolated pathogenic Leptospira bacterium - useful; eveloping products for conferining protective immunity, robehylactic or therapent for transment	
GenCore v (c) 1993 - , using sw 2001, 08:22 326A-5	Gapop d: 480025 Jmber of hits se DB seq length:	DB sed le	Database : N_Geneseq_36:*	7 100.0 15 16 7 100.0 15 16

98US-0111715.

08-DEC-1998;

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  This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainel. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and diagnosis of past or present LS infection.
                                                                                                                                                                                                                                                                                                                                                              SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
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                                                                                                                                             Length 7;
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                                                                                                                                          100.0%; Score 7; DB 19; I
100.0%; Pred. No. 5.2e+07;
Live 0; Mismatches 0;
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                                                                                                           Sequence 7 BP; 2 A; 0 C; 1 G; 4 T; 0 other;
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Sequences 27573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding cypressed in monocyte-derived dendritic cells compared differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while preferentially or differentially expressed in dendritic cells, while correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cell chart continuous antigen presentation via the MRC (major histocompetability complex) and subsequent recognition by T-cell receptors is alone complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytocoxic immune response that can lyse complex) and subsequent recognition by Cofactors also being required for the tumour cells, immunostimatory refactors also being required for sequences; identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to induce an immune response, particularly adainst a tumour antigen to modulate the genotype of an APC; confidential users, or of their encoded proteins, can be used to dentify expressed genes, or of their encoded proteins, can be used to an expression of these genes. Detection of the dentitic cell differentially expressed genes, or of their encoded proteins, can be used to antigen specific effector cells and become antigen specific effector cells and each of antigen-specific effector cells and each of antigen-specific effector cells, and vectors containing the propulation of antigen-specific effector cells, and vectors containing to the mare used in active immunotherapy (or to stimulatory factors ensures adequate antigen presentation 
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                                                                                                                                                                                                                  Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer .
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                  Roberts BL, Shankara
                                        (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
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that are preferentially transcribed in the metastatic breast tumour that are preferentially transcribed in the metastatic breast tumour cells). Issue (i.e. are upregulated in metastatic breast tumour cells). Edsignate to 286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Or of preferential modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, or e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or call-based vaccines; for diagnosing breast cancer and for raising specific cantibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agenticals that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter fumnor became the polypeptides can be used to expand the paracells that produce the polypeptides can be used to expand the metastatic calls, e.g. cytotoxic T lymphocytes, and these used for adoptive
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Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim'1; Page 60; 219pp; English.
                                                                                                                                                                                                   98US-0089853.
98US-0089997.
98US-0090039.
98US-0090040.
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                                                                                                                                                          99WO-US13647
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Roberts BL, Shankara S;
                                                                                                                                                                                                                                                                                                                                                 (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
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                                                                                                                                                                                                                                                                                                                                                                                                (SHAN/) SHANKARA S.
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                   Homo sapiens.
                                                               WO9965928-A2
                                                                                                                                                                                                      19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
                                                                                                                                                       18-JUN-1999;
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Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.

Metastatic breast tumour cell upregulated transcript tag #2351.

07-APR-2000 (first entry)

283117;

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Tablo 10 28391 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour cells). 283942 tepresent tags corresponding to distinct transcripts that are to 286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific continuousles (Ab). Ab are used to detect the polypeptides or as therapeutic agentic. Host cells that produce the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter immune breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280767 to 283941 represent tags corresponding to distinct transcripts
                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer -
                                       Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
           Metastatic breast tumour cell upregulated transcript tag #2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 BP; 4 A; 0 C; 2 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 113; 219pp; English.
                                                                                                                                                                                                                            98US-0089997.
98US-0090039.
98US-0090040.
98US-0090041.
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                      Roberts BL, Shankara S;
                                                                                                                                                                                                                                                                                             (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-106079/09.
                                                                                                                                                                                                                                                                                                                          (SHAN/) SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunotherapy
                                                                                                                          WO9965928-A2.
                                                                                                 Homo sapiens
                                                                                                                                                                                  18-JUN-1999;
                                                                                                                                                                                                                                                        19-JUN-1998;
                                                                                                                                                                                                             19-JUN-1998
                                                                                                                                                      23-DEC-1999
                                                                                                                                                                                                                             19-JUN-1998
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Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer -

Roberts BL, Shankara S;

WPI; 2000-106079/09.

(GENZ ) GENZYME CORP. ROBERTS B L.

(ROBE/) ROBERTS B L (SHAN/) SHANKARA ·S.

98US-0089997. 98US-0090039. 98US-0090040.

19-JUN-1998; 19-JUN-1998; 19-JUN-1998; 19-JUN-1998;

99WO-US13647 98US-0089853

18-JUN-1999; 23-DEC-1999

19-JUN-1998

WO9965928-A2. Homo sapiens

Claim 1; Page 122; 219pp; English.

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that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). 283942

tissue (i.e. are upregulated in metastatic breast tumour cells). 283942

to 286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, cell e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides or as therapeutic agents. Host cells that produce the polypeptides on be used to expand and isolate populations of educated, antigen-specific immune effecter immuncherse.
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280767 to 283941 represent tags corresponding to distinct transcripts
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Best Local Similarity 100.0
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tttgata 7
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RESULT

Z83117 standard; DNA; 10 BP.

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Gaps

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Length 10; 0; Indels

100.0%; Score 7; DB 21; I 100.0%; Pred. No. 1.9e+04;

Mismatches

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us-09-380-826a-5.rng

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rb gene; antisense oligonucleotide; modulate; gene expression; ss
                                      Homo sapiens
                                                                                                            31-JAN-1997;
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                                                             EP856579-A1
                                                                                    05-AUG-1998.
                                                                                                                                                                                  Brysch W,
                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes the detection of drug-selected mutations in the HIV protease gene. The method of detection allows the simultaneous characterisation of a range of codons involved in drug resistance using sets of probes optimised to function together in a reverse-hybridisation assay. 297517 to 297997 represent specifically claimed probes for use in che assay, and 29479 to 297501 represent specifically claimed HIV protease gene polymorphic nucleotide sequences. 297502 to 297515, and 298004 to 298007, represent PCR Finers for the HIV protease gene, and 297516 represents an HIV protease probe used in an example from the cresent invention. The method, probes and primers can be used for the detection of drug selected mutations in the HIV protease gene. The method allows the simultaneous characterisation of a range of codons involved in drug resistance. The method may also be used for HIV protease genotyphing assays. The probes are able to discriminate between wild type and mutated protease sequences. The method allows rapid and
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                                                                                                         Human immunodeficiency virus; HIV; protease; probe; detection; drug selected mutation; hybridisation; genotyping; infection; drug resistance; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reliable detection of drug-selected mutation in HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13 BP; 5 A; 1 C; 2 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rb gene antisense oligonucleotide rb-N-103
                                                                                    HIV-1 protease gene probe SEQ ID NO:209.
                                                                                                                                                           Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 37; 76pp; English.
297719/c
ID 297719 standard; DNA; 13 BP
                                                                                                                                                                                                                                                           98EP-0870143.
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                                                           26-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                   (INNO-) INNOGENETICS NV
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                                    297719;
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V49155
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consecutive cytosines; do not contain two sequences of three consecutive nuclectides each able to form three H bonds to three consecutive cytosines, and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The oligonoclectides are used to modulate expression of genes, particularly the genes for p53, ErB-2, junB, junD, 7GF-beta 1 or beta 2 to control proliferation of primary cell cultures (e.g. bone marrow stem, liver or bigonuclectides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically e.g. in cases of cancer or (targeting TGF) for stimulating the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the rb gene. Of these, only oligonucleotides V49008-52 regulted in effective downregulation of negative growth control by rb, while oligonucleotides V49052-236 had little effect. The oligonucleotides exemplify the invention. The specification describes oligonucleotides that contain 8-30 nucleotides, which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and reduced toxicity, used therapeutically or to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V49008-236 represent antisense oligonucleotides directed against
                                                                                                                                                                                                                                                                                                                                                                                                                        consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                    Preparation of antisense oligo:nucleotide(s) which lack long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 7; DB 19; 1 100.0%; Pred. No. 1.8e+04;
                                                                                                                                                    (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14 BP; 5 A; 1 C; 1 G; 7 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Fig 9c; 286pp; English.
                                                                                                                                                                                                                                Schlingensiepen K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11/c
297691 standard; DNA; 14 BP.
97EP-0101531
                                                                            97EP-0101531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth of cells in culture
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Best Local Similarity 100.
Matches 7; Conservative
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1 tttgata 7
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920S-093610 920S-0936421 920S-0936422 920S-0936531 920S-0936532 920S-0936131 930S-0006122

93WO-US04573 32US-0882822 32US-0882885

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New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated with tumours or mRNA expressed from gene encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              multiple drug resistance
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                                                                    13-MAY-1993;
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   25-NOV-1993.
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       DAY BARRARA KARANA KARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the HIV protease gene. The method of detection allows the simultaneous characterisation of a range of codons involved in drug resistance using sets of probes optimised to function together in a reverse-hybridisation assay. 297517 to 297997 represent specifically claimed probes for use in the assay, and 297479 to 297501 represent specifically claimed HIV protease gene polymorphic nucleotide sequences. 297502 to 297515, and 297516 represents an HIV protease gene, and 297516 represents an HIV protease probe used in an example from the present invention. The method, probes and primers can be used for the method allows the simultaneous characterisation of a range of codons involved in drug resistance. The method may also be used for HIV protease genotyping assays. The probes are able to discriminate between all drug appropage genotyping assays. The probes are able to discriminate between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes the detection of drug-selected mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver; resistance; chemotherapeutic agent; colchicine; doxorubicin; colon; actinomycin D; vinblastine; small intestine; kidney; adrenal gland; adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia; human; chronic myelogenous leukemia; CML; follicular lymphocytic leukemia; b=cell acute lymphocytic leukemia; meuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif; hairpin; hepatitis delta virus; group I intron; RNaseP; leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of drug-selected mutations in the HIV protease gene used to treat HIV infections \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The method allows rapid and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wild type and mutated protease sequences. The methor reliable detection of drug-selected mutation in HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 7; DB 21; I
100.0%; Pred. No. 1.8e+04;
Live 0; Mismatches 0;
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Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 37; 76pp; English.
                                                                                                                                                                                                        99WO-EP04317.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-147219/13.
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                                                            W09967428-A2
                                                                                                                                                                                                    22-JUN-1999;
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                                                                                                                                    29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                             Stuyver L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              052243;
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The sequences given in Q51825-2266 represent areas of mRNAs which are associated with development or maintenance of chronic myelogenous leavenia (CML), promyelocytic leukemia, Burkit's lymphoma, or cluck lymphocytic leukemia, follicular lymphoma, B-call acute lymphocytic leukemia, follicular lymphoma, B-call acute lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer. The full length mRNAs contraining these target caquences, encode aberant cellular proteins which are able to control cellular proliferation and are directly linked to a leukemic phenotype. These target sequences are identified by the ribozyme of the invention. The ribozymes is formed in a hammerhead motif, but may also be formed in the motif of a hairpin, hepatitis delta virus, group I intron or RNasep-like RNA. These ribozymes may be used to infiliat chere animals by modulating expression of the corresponding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage of target mRNAs expressed in pre-neoplastic and transformed cells elicits inhibition of the transformed state. Multiple drug resistance (mdr-1) mRNA specific ribozymes remove the mechanism of drug resistance used by transformed cells and thus enhances drug therapies for tumours. The ribozymes may also be used to study genetic drift and mutations within cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 7; DB 14; Length 15; 42.9%; Pred. No. 1.8e+04; Live 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 4 A; 1 C; 1 G; 9 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 42.9%;
Matches 3; Conservative
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T56960
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Homo sapiens

WO9323057-A.

us-09-380-826a-5.rng

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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves mRNA coding for a protein of respiratory syncytial virus (RSV) at the nucleotide base position indicated in the DE line. Regions of the manna that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the target sequences and can be used for treatment and diagnosis of
                                                                          atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human Immunodeficiency virus; acquired immune deficiency syndrome;
     RSV; bcr-abl; oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
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Grimm S, Karpelsky A, Kisich K, Matulic-Adamic J;
McSwiggen JA, Modak A, Pavco P, Beigelman L, Sullivan SM;
Sweedler D, Thompson JD, Tracz D, Usman N, Wincott FE;
TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncoctranslocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 269; 407pp; English.
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940S-021109-940S-0201109-940S-0222795.
940S-02227958-940S-0227958-940S-0227958-940S-0291932-940S-039139-940S-0311486-940S-03114897-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-03134847-940S-031334847-940S-031334847-940S-031334847-940S-031334847-940S-031334847-940S-031334847-940S-031334847-940S-0313337-940S-0313337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-031323337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-031323337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S-03132337-940S
                                                                                                                                                                                                                                  Respiratory Syncytial Virus
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                                                                                                                                                                                  AIDS;
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Sequence 15 BP; 7 A; 0 C; 3 G; 5 U; 0 other;

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Gaps
                                                                                                                                                                                                                                                  gene expression; downregulation; interleukin-5; IL-5; ICAM-1; Intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; trans.Location; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rhewmatoid arthritis; psoriasis; myocardial ischeemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LM; Grimm S, Karpetsky A, Kisich K, Matulic-Adamic J; McSwiggen JA, Modak A, Pavco P, Beigelman L, Sullivan SM; Sweedler D, Thompson JD, Tracz D, Usman N, Wincott FE;
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                                                                                                                                                                                                                                         Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
                                                                                                                                                                                                                 RSV 1C hammerhead ribozyme target sequence (nt. position 17).
             Length 15;
Score 7; DB 16; Length 15;
Pred. No. 1.8e+04;
                                   4;
            100.08;
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94US-0218934.
94US-0222795.
                       42.98;
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94US-0311486
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94US-0227958
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Query Match
Best Local Similarity 42...
Secondary 3; Conservative
                                                                                                                                            T56962 standard; RNA; 15
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29-MAR-1994;
04-APR-1994;
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15-APR-1994;
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T56962
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                                                                                             The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves mRNA coding for a protein of respiratory syncytial virus (RSV) at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the target sequences and can be used for treatment and diagnosis of
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
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                                          pzymes having modified bases and methods for producing them use in inhibiting disease related genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSV 1C hammerhead ribozyme target sequence (nt. position 21).
                                                                                                                                                                                                                                                              Length 15;
                                                                                                                                                                                                                                                             ; Score 7; DB 16; Length 15
Pred. No. 1.8e+04;
4; Mismatches 0; Indels
                                                                                                                                                                                                                               Sequence 15 BP; 7 A; 0 C; 3 G; 5 U; 0 other;
                                                                           Claim 2; Page 269; 407pp; English
                                                                                                                                                                                                                                                              100.0%;
42.9%; F
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94US-0245736.
94US-0271280.
94US-0291932.
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94US-0218934
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                                            Ribozymes
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  Woolf T;
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T56964
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves mRNA coding for a protein of respiratory syncytial virus (RSV) at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the trarget sequences and can be used for treatment and diagnosis of
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Pred. No. 1.8e+04;
1; Mismatches 0;
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ID T57424 standard; RNA; 15 BP.
94US-0292620.
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transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
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Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J;
WcSwiggen JA, Modak A, Pavco P, Beigelman L, Sullivan SM;
Sweedler D, Thompson JD, Tracz D, Usman N; Wincott FE;
Woolf T;
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9405-022795
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                                                               Respiratory Syncytial Virus
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gene expression; downrequation; interleukin-5; IL-5; ICAN-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpèisky A, Klsich K, Matulic-Adamic J; McSwiggen JA, Modak A, Pavco P, Belgelman L, Sullivan SM; Sweedler D, Thompson JD, Tracz D, Usman N, Wincott FE;
                                                                                                                                                     RSV N hammerhead ribozyme target sequence (nt. position 1148).
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94US-0334847
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T57425 standard; RNA; 15
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                      13 TTTGATA 7
tttgata 7
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Woolf T;
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23-DEC-1994;
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Gaps

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Query Match 100.0%; Score 7; DB 16; I Best Local Similarity 100.0%; Pred. No. 1.8e+04; Matches 7; Conservative 0; Mismatches 0;

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PT Ribozymes having modified bases and methods for producing them - xx xx Claim 2; Page 276; 407pp; English.

XX Claim 2; Page 276; 407pp; English.

CC The present sequence represents a preferred target sequence for an enzymatic nucled; a ribozyme) which cleaves mRNA coding CC for a protein of respiratory syncytial virus (RSV) at the contectide base position indicated in the DE line. Regions of CC the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites contain potential hammerhead and hairpin ribozyme sites contain man sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the target sequences and can be used for treatment and diagnosis of XX Sequence 15 BP; 6 A; 4 C; 2 G; 3 U; O other;
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Query Match 100.0%; Score 7; DB 16; Length 15; Best Local Similarity 100.0%; Pred. No. 1.8e+04; Matches 7; Conservative 0; Mismatches 0; Indels Qy 1 tttgata 7

Qy 1 tttgata 7

Db 11 TTGATA 5

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Job time: 5301 sec

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/cgn2_6/ptodata/2/ina/PCTUS.COMB.seq:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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AP A		. 6
2320, Ap 2321, Ap 25, Appli 7, Appli 8, Appli 820, App 1561, Ap 2411, Ap 2567, Ap 2567, Ap 2567, Ap 2567, Ap	. p	Sdeb
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US-08-585-6848-2320 US-08-584-6848-2321 US-08-634-560-25 US-08-930-917A-8 US-08-930-917A-8 US-08-937-124A-522 US-08-373-124A-1561 US-08-373-124A-1563 US-08-373-124A-2411 US-08-373-124A-2413 US-08-373-124A-2555 US-08-373-124A-2555 US-08-373-124A-2555 US-08-373-124A-2555 US-08-373-124A-2555 US-08-373-124A-2555 US-08-373-124A-2555 US-08-373-124A-2555 US-08-435-628-520 US-08-435-628-520 US-08-435-628-1563	Alloantigen	B 1; Length 11 .1e+03; .s. 0; Indels
-6848- -350-2 -350-2 -917A- -124A- -124A- -124A- -124A- -124A- -124A- -628-5	US/08086634 US/08086634 Sentot Saleh Molecular Basis of the Human Platelet Bra/Brb Applications Thereof 12 SS: & Lardner 1497 RM: Py Disk compatible Py Disk compatible Py Disk compatible The Compatible Py Disk warions 1497 RM: 1497 RM: RM: 130,136 UNG: 6: 111am J. 113am J. 115am J.	; D 0. 7 tche
88 - 58 88 - 58 88 - 58 88 - 58 88 88 - 58 88 88 - 58 88 88 88 88 88 88 88 88 88 88 88 88	ALIGNMENTS  eh Baais of the elet Bra/B on 5.1  6,634  6,634	Score 7 Pred. N Misma
	Peter J. Peter J. Sentot Saleh Molecular Basis Human Platelet E Applications The SSS: E Lardner 1497 PC-MOS/MS-DOS PC-DOS/MS-DOS PC-DOS/MS-DOS PC-DOS/MS-DOS PC-TOS/MS-DOS PC-TOS/MS-DOS FC-T, Version 5.1 DATA: AMATION:	ä
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15 115 116 117 117 117 117 117 117	N: AN, Peter J. Soloto US/080866 N: AN, Peter J. Soloto Sentor Soloto N: Human Pla ON: Human Pla ON: Human Pla ON: Human Pla DDRESS: Ley & Lardner Box 1497 Sin 97 F. FORM: F. WHILLIAM J.	ä
000000000000000000000000000000000000000	a Ozerherzeu .cc 47 zenep hezmonogeneo c	h Similarity 100 7; Conservative tgata 7 1 1 11
	SULT 1  -08-086-634-6/c Sequence 6, Applicat, Sequence 5.516634  APPLICANT: NEWMAN APPLICANT: SANTO TITLE OF INVENTION TOPPERSENCE AD STATE: WAGAISON STATE: WAGAISON STATE: WAGAISON COMPUTER: IBM OPERATION STATE SOFTWARE: WORD CURRENT APPLICATION FILING DATE: 3 ATTORNEY/AGENT IN REFERENCE/DOCKE TELEPHONE: (608) INFORMATION FOR SEQ SEQUENCE CHARACTE TELEPHONE: (608) INFORMATION FOR SEQ SEGUENCE CHARACTE TELEPHONE: (608) INFORMATION FOR SEQ SEGUENCE CHARACTE TELEPHONE: (608) INFORMATION FOR SEQ SEGUENCE CHARACTE LENGTH: I DAS TYPE: CCANACTE TOPPLOGGY: LINE	tt TI
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OPERATING SYSTEM: IBM P.C. DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/166,664 FILING DATE:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRASEQ VERSION 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/271,880A FILING DATE: July 7, 1994
PRIOR APPLICATION DATA: including app PRIOR APPLICATION DATA: described belanger APPLICATION DATA: 08/103,243
                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/884,074
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAFDURG, RICHARD 32,327
REFERENCE/DOCKET NUMBER: 197/062
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 217, Application US/08271880A
; Patent No. 5693535
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     August 6, 1993
UMBER: 07/882,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street'
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
US-08-166-664-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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US-08-271-880A-217/c
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                                                                  US-08-08-08-034-07-05

Sequence 7, Application US/08086634

Patent No. 5516634

GENERAL INFORMATION:

APPLICANT: SANTOSO, Sentot Saleh
TITLE OF INVENTION: Molecular Basis of the
TITLE OF INVENTION: Human Platelet Bra/Brb Alloantigen System and
TITLE OF INVENTION: Homen Platelet Bra/Brb Alloantigen System and
TITLE OF INVENTION: Homen Platelet Bra/Brb Alloantigen System and
TITLE OF INVENTION: Human Platelet Bra/Brb Alloantigen System and
TITLE OF INVENTION: Human Platelet Bra/Brb Alloantigen System STREET: P. 0. Box 1497

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STAME: Wadison
STAWE: Wadison

COUNTRY: Madison

STAWE: Wisconsin
COUNTRY: Sayol-1497

COMPUTER READALE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER: 1BM FC COMPATION:

MEDIUM TYPE: Floppy Disk
COMPUTER: 30-June-1993

ATTORNEY AGENT INFORMATION:

RESPERANCE SCANION, WHILliam JO. 136

REPERBENCE SCANION INFORMATION:

REGISTRATION INFORMATION:

RELEPHONE: (608) 258-4284

INFORMATION FOR SED ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 Dase pairs

LENGTH: 11 Dase pairs

LENGTH: 11 Dase pairs
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Patent No. 5646020

GRNERAL INFORMATION:

APPLICANT: James A. McSwiggen

APPLICANT: J. Anthony Mamone

TITLE OF INVENTION: HAMMERHEAD RIBOZYMES FOR

TITLE OF INVENTION: PREFERRED TARGETS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1e+03;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 1;
Pred. No. 7.1e+0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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US-08-166-664-5/c
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                                        RESULT 2
US-08-086-634-7/c
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Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Renneth G. Draper
APPLICANT: Bharat Chownira
APPLICANT: Bharat Chownira
APPLICANT: James McSwigora
APPLICANT: James D. Thompson
ITILE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION: REPLICATION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       appplication
below:
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Gaps
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Dan T. Stinchcomb
James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
HUMAN IMMUNOBETCIENCY VIRUS
REPLICATION
                                                                                                                                                          Length 13;
                                                                                                                                                                                               0; Indels
                                                                                                                                                      DB 2;
7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,215
FILING DATE: 12-Feb-1999
PRIOR APPLICATION NUMBER: 08/910,408
FILING DATE: AUNTOWND
APPLICATION NUMBER: 08/910,343
FILING DATE: AUNTOWND
APPLICATION NUMBER: 07/882,886
APPLICATION NUMBER: 07/882,886
APPLICATION NUMBER: 07/882,886
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ 1D NO: 217: US-09-249-215-217
                                                                                                                                                      Query Match 100.0%; Score 7; Best Local Similarity 100.0%; Pred. No. Matches 7; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                      Sequence 217, Application US/09249215 Patent No. 6159692 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kenneth G. Draper
Bharat Chowrira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 217:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
  SEQUENCE CHARACTERISTICS
                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                linear
                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-09-249-215-217/c
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US-08-910-408-217
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Patent No. 5972704
GENERAL INFORMATION:
APPLICANT: Reneth G. Draper
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION: REPLICATION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 DB 1; Length 13; 7e+03;
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 90071
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,408
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/271,880
FILING DATE: July 7, 1994
APPLICATION NUMBER: 08/103,243
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 23,327
REFERENCE/DOCKET NUMBER: 206/116
TELECOMMUNICATION INFORMATION:
                                                         206/116
        NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/J
RELECOMMUNICATION INFORMER: 206/J
TELEPHONE: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 217:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (213) 489-1600
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (213) 955-0440
                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & L. STREET: 633 West Fi STREET: Sulte 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-271-880A-217
                                                                                                                                                                                                                                                                                                                                                                                                                                10 TTTGATA 4
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Renneth G. Draper
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: Dan T. Stinchcomb
APPLICANT: Dan T. Stinchcomb
APPLICANT: Dan T. Stinchcomb
TITLE OF INVENTION: HUMAN IMMUNOBERICIENCY VIRUS
TITLE OF INVENTION: REPLICATION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 7; DB 2; Length 14; 100.0%; Pred. No. 7e+03; usemarches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: 1EM COMPATIBLE
OPERATING SYSTEM: 1EM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,408
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRICE DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/271,880
FILING DATE: July 7, 1994
APPLICATION NUMBER: 08/103,243
FILING DATE: MAUST 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: MAY 14, 1992
ATORNEY/AGENT INFORMATION:
NAME: WARDLEY, RACHARD
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELERAX: 67-3510
INFORMATION FOR SEQ ID NO: 212:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 212, Application US/09249215; Patent No. 6159692; GENERAL INFORMATION:
APPLICANT: Kenneth G. Draper
Bharat Chowrira
James McSwiggen
Dan T. Stinchcomb
                            Sequence 212, Application US/08910408
Patent No. 5972704
                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
Lac 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                      STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 tttgata 7
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US-09-249-215-212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90071
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                                              Gaps
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                                                                                                                                                                                                                                                     APPLICANT: Kenneth G. Draper
APPLICANT: Bharat Chowria
APPLICANT: Bharat Chowria
APPLICANT: James McSwiggen
APPLICANT: James D. Thompson
APPLICANT: James D. Thompson
TITLE OF INVENTION: HUBAN IMMUNOBERICIENCY VIRUS
TITLE OF INVENTION: HUBAN IMMUNOBERICIENCY VIRUS
TITLE OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Wast Fifth Street
STREET: Galifold
CITY: Los Angeles
STATE: Califold
CONTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 7; DB 1; Length 14; Best Local Similarity 100.0%; Pred. No. 7e+03; Matches 7; Conservative 0; Mismatches 0; Indels
Length 13;
                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,880A
FILING DATE: July 7, 1994
PRIOR APPLICATION DATA: including appplication
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/116
TELEPHONE: (213) 489-1600
TELEPRIOR: (213) 955-0440
TELERX: 67-3510
TELERX: 67-3510
INFORMATION FOR SEQ ID NO: 212:
FRACTH. 14 base pairs
    core 7; DB 3; Ired. No. 7e+03; Mismatches 0
    100.0%; Score 7; 100.0%; Pred. No.
                                                                                                                                                                                                                                            Sequence 212, Application US/08271880A
Patent No. 5693535
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
         Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 tttgata 7
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3 TTTGATA 9
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                                                                                             1 tttgata 7
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TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: BELATED TO LEVELS OF
TITLE OF INVENTION: NF-AB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                 COMPUTER: SUCIONAL TREES: SUCIONAL TREES: SUCIONAL TREES: WORE SUCIONAL TREES: WORLD BATC. DOS 5.0 SOFTWARE: WORLD PERCET 5.1 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A FILING DATE: BANDER: 08/25,466
FILING DATE: RAY 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: FEBRUARY 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: DECEMBER 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: DECEMBER 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: DECEMBER 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: MAUSE 18, 132,32
ATTORNEY/AGENT INFORMATION:
NAME: WARDING, RICHARD
REGISTRATION NUMBER: 32,327
PERFEDENCE/TOCKER MIMMED: 2006/036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 7; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUWTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 129, Application US/08291932A Patent No. 5658780 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209/035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: MCSwiggen, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (213) 499-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
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Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                       Los Angeles
California
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                                                                 U.S.A.
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US-08-291-932A-129
                                                                                 90071
                                          STATE: CA
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James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
HUMAN IMMUNOBELCIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 7; DB 3; Length 14; 100.0%; Pred. No. 7e+03; ive 0; Mismatches 0; Indels
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US-08-373-124A-90/C
US-08-373-124A-90/C
US-08-373-124A-90/C
Sequence 90, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Daryer, Kenneth
APPLICANT: Daryer, Kenneth
APPLICANT: Daryer, Thale
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,215
FILING DATE: 12-Feb-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION UNMBER: 08/910,408
FILING DATE: «CURKNOWN)
APPLICATION NUMBER: 08/103,243
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: MAY 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/116
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 212: US-09-249-215-212
                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 212:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                      NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 90071
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Pred. No. 7e+03;
; Mismatches 0; Indels
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PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
APPLICATION NUMBER: 07/987,132
APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSaviggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPOTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
               FILING DATE: Way 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY-AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECHONE: (213) 489-1600
TELEFRAM: (213) 955-0440
TELEFRAM: (213) 955-0440
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 131, Application US/08291932A patent No. 5658780 GENERAL INFORMATION:
  08/245,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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42.9%; F
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REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                 LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RY: U.S.A.
90071-2066
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7 UUUGAUA 13
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US-08-291-932A-130
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                                                                                                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
APPLICATION NUMBER: 07/987,132
APPLICATION TO THE PROPRESSION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: MCSAY49Gen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NP-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 7e+(
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IDM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/291,932A FILING DATE: Aqqust 15, 1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-291-932A-130
Sequence 130, Application US/08291932A
Patent No. 5558780
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/COCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPRAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; 42.9%; 1
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TELEFAX: (713,
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12'
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
LENGTH: 15 base pairs
""SE: nucleic acid
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 3; Conserv
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90071-2066
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9 UUUGAUA 15
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          Indels
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          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; DB 1;
Pred. No. 7e+03;
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INHIBITING RESPIRATORY TITLE OF INVENTION: SYNCTIAL VIRUS NUMBER OF SEQUENCES: 909 CORRESPONDENCE ADDRESS: ADDRESSE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WOR'D PORTECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/334,847
FILING DATE: No. 5693532ember 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: March 27, 2001, 08:19:22 Job time: 5149 sec
                                                                                                                                                                               ; Sequence 9, Application US/08334847
; Patent No. 5693532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J.
REGIGSTRATTON NUMBER: 32,327
REERENCE/CDCKET NUMBER: 209/TELECOMMUNICATION INFORMATION:
TELEPAN: (213) 489-1600
TELEPAN: (213) 955-0440
IEEEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
          4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MCSwiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pam
APPLICANT: Woolf, Tod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 42.9.
Teches 3; Conservative
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LENGTH: 15 base pairs
        .3; Conservative
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STRANDEDNESS: single
                                                                                   7 UUUGAUA 13
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6 UUUGAUA 12
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                                            1 tttgata 7
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US-08-334-847-9
        Matches
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                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08334847
Patent No. 5693532
GENERAL INFORMATION: APPLICANT: McSwiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: SINCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 18 Compatible
OPERATING SYSTEM: 18M P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
RILING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                          Pred. No. 7e+(
4; Mismatches
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TELEPHONE: (213) 489-1600
TELERA: (213) 955-0440
TELEX: (67-3510
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANBENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 209/,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                      100.0%;
42.9%; F
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TELEFAX: (213) 955-0440
TELER: 67-3510
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 42.9
Matches 3; Conservative
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EDNESS: single
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Best Local Similarity
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6 UUUGAUA 12
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US-08-291-932A-131
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US-08-334-847-8
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9b_est47::

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9b_est50::

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9b_est51::

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                                                                                                                            March 27, 2001, 07:38:21 ; Search time 2517.78 Seconds
  (without alignments)
  19.482 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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gb_est6:**

gb_est6:**

gb_est10:**

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Perfect score:
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AZ329387 IM0032C01
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AZ345476 IM0030EP11
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AU008929 AU008929
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R98634 Y469906.T1
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AU012255 AU12255
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AZ42862 IM021255
AZ42862 IM0210.S
AZ42862 IM021005995
C21092 IM02500266
E286538 YFS80951
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1M0045A01R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0045A01 R, DNA sequence.
AZ323820
AZ323820.1 GI:10378917
GSS.
house mouse.
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AZ329387 1M0053C07
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AA226145 nc09f09.r
AA846437 a185c09.s
                                                                             pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                         Description
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27 A1073656
28 A1073656
29 A1073656
172 AZ47488
173 AZ47488
170 AZ36364
172 AZ411435
148 AQ025283
171 AZ49183
28 AU008005
28 AU00805
28 AU012255
10 AA692338
172 AZ423769
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AZ407162
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase and T4 polymerase and T4 high majar excess. The shate to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114[plbAFL29072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for amplcillin resistance."
                                                                                                                                                                                                                                                                              plasmid inserts
Uppublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Emil: ddundegenetics.utah.edu
Emil: ddundegenetics.utah.edu
                                                                                        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Dunn, D., Aoyad, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1M0342C04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0342C04 R, DNA sequence.
AZ502952
AZ502952.1 GI:10684268
                                   Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                         Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 10000 Std Error: C
Plate: 0053 row: C column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/db_xref="taxon:10090"
/clone="UUGC1M0053C07"
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Location/Qualifiers
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G75BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114[gb]AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                      plasmid inserts
Unpublished (2000)
Contact: Nobert B. Weiss
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Walss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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AZ329387.1 GI:10390050
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                                                                                                                                                                                                                                                                                                                                                                                             Rm. 308, Biomedical Polymers Research Bld 4112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 005 Frow: A column: 01 Seg primer: CACACAGGAACAGCTATGACC Class: plasmid ends
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Fm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                       Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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//lab_host="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
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Location/Qualifiers
AZ345476.1 GI:10424713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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23 TTTGATA 17
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                                                                            Bukaryota; Metazoa; Chordata; Craniatá; Vertebrata; Euteleostomi; Makaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0342 row: C column: 04
Seq primer: CACACAGGAAACAGCTATGACC
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide Kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwn42 (qi|4732114|qplART29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 7; Conservative 0; Mismatches 0;
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ORGANISM

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) gblaF129072.1), a copyrnumber inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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                                                                                                                                                        Mus musculus
Eukaryota, Metzoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
iM., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
/lab.host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                Mouse whole genome scaffolding with paired end reads from 10kb
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/clone="luQC1M0302P17"
/clone=lib="Mouse 10kb plasmid UUGC1M library"
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100.0%; Score 7; DB 173; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0302 row: P column: 17
Seq primer: CGTGTAAAAGGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
      clone UUGC1M0302P17 F, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb.
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (2.24)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Aslam, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 801 JOD (27)
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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/organism="Mus musculus"
/strain="C57BL/6J"
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Plate: 0134 row: M column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
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A2379215.1 GI:10492915
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Fax: 801 585 7177
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Mus musculus
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Email: staben@pop.uky.edu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="spc04231"
/clone="hb="schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/note="vector: M13mp19; The cDNA library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)
Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                  Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
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AU008929 Schizosaccharomyces pombe late log phase CDNA
Schizosaccharomyces pombe CDNA clone spc04231, mRNA sequence.
                                                                                                                                                                                                                                                              Unpublished (1998)
Contact: Mitsucki Morimyo
Contact: Mitsucki Morimyo
Genome Research Group
National Institute of Radiological Sciences
National Institute of Radiological Sciences
P-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
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                                                                                                                       Schizosaccharomyces pombe
Eukaryota; Fungi, Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.

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/organism="Schizosaccharomyces pombe"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
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Importatory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared bNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5. to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gil4732114 (gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampliallin resistance."
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Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C., Edman, J.C., Kovacs, J. and Cushion, M.
Expressed sequence tags from Pneumocystis carinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
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Pneumocystis carinii f. sp. carinii
Eukaryota; Fungi; Fungi incertae sedis; Pneumocystidaceae;
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/clone="wcC1M0171120"
/clone=lib="Wouse lOkb plasmid UUGCIM library"
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                               0.00
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0173 row: L column: 20
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
High quality sequence stop: 25.
                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
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Fax: 606 257 1717
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end replated with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwad (gil4732114(gblAF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
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1M0065E13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0065E13 R, DNA sequence.
                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B. Welss
Contact: Robert B. Welss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 Low: D column: 24
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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Location/Qualifiers
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AZ328549.1 GI:10388388
GSS.
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                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 27)
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                                                                               /clone_lib="AGS:1"
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P. carini organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/1/799) at Cincinnati VA facilities.
Trizol extracted RNA Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara
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Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K. Analysis of gene expression in mouse embryogenesis by 3'-directed control and sequencing.
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    26
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/db_xref="taxon:38081"

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Pred. No. 2.2e+05;
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3-1 Yamada-oka, Suita, Osaka 565, Japan.
Location/Qualifiers
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Mus musculus domesticus
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Schizosaccharomyces pombe cDNA clone spc02033, mRNA sequence.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114 gbjAR129072.1), a copy-number
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adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                       Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

WR. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Bukaryotas, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi,

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 27)

Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib-"Mouse 10kb plasmid UUGC1M library"
/sex-"Male"
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Insert Length:.10000 Std Error: 0.00
Plate: 0065 row: E column: 13
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
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/clone="UUGC1M0065E13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 30)

S NIH-WGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onbublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Contact: Robert Strausbergenih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CONA Library Preparation: Life Technoologies, Inc.

CDNA Library Preparation: Life Technoologies, Inc.

CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LNL at:

http://mage.llnl.gov
Plate: LLAM9128 row: f column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of Ml3mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jb)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Schizosaccharomyces pombe"
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/clone="spc02033"
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/sex="h minus"
/note="Vector: Ml3mp19; The cDNA library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE911076 30 bp mRNA EST 29-SEP-2000 601662175F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3962130 5',
                                                                                                                                                1 (bases 1 to \hat{30}) Morimyo,M. and Mita,K. Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                Genome Research Group Antional Institute of Radiological Sciences National Institute of Radiological Sciences 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan Email: morimyo@nis.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
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fission yeast.
Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                Contact: Mitsuoki Morimyo
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us-09-380-826a-5.rst

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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Glibert Smith, NIH"

12 a 1 c 4 g 13 t
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Tel: 06-877-5111(ex.3315)
Email: Kousaku@incb.osaka-u.ac.jp
Human Gene Signature, 3'-directed cDNA sequence. We are not:
submitting the same cDNA sequence redundantly to DDBJ since 1993.
For the abundance information of clones with this sequence in this
library and as well as in other 3'-directed libraries, see '
http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones
represented by this GS sequences is also found there.
Location/Qualifiers
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 30)
6 (bubo,K.
BodyMap; human gene expression database
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HUMGS0004973 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
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C20899
C20899.1 GI:1622009
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Search completed: March 27, 2001, 07:38:23 Job time: 4586 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                            March 27, 2001, 08:17:04; Search time 2286.42 Seconds (Without alignments) 49.243 Million cell updates/sec
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        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AF051649 Homo sapl.
M95263 Human chrom
G50458 SHGC-79916
D38547 Small round
AJ009225 Bos tauru
AJ009229 Homo sapl
AJ009223 Bos tauru
U52077 Human marin
U60594 Leptospira
U66913 Dictyosteli
X89236 S.pyogenes
A45819 Sequence 13

BTAJ9224 BTAJ9223 HSU52077 LFU60594

533 233 335 335 337 337 337 337 337 337 337

1015 1257 1257 1258 1276 1287 1481 23321 2683 3666

Description

SUMMARIES

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HSSSG03 HUM4 STS161 G50458 SRSSRSV BTAJ9225 HSAJ9229

A45819 Sequence 13 A45820 Sequence 14 249313 S. Cerevisia A45813 Sequence 7 A45814 Sequence 8 249320 S. Cerevisia U36757 Ms musculu AC014767 Drosophil

DDU66913 SPGROELGN A45819 A45820 SCYJL046W A45813

SCYJL045W MMTHREC02

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ENKATYCKE, METAZOA; Chordata; Craniata; Vertebrafa; Euteleostomi; EnklaryCta; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)

1 (bases 2 to 435)

2 (boold, R.D., distabloog, Xu, H., Lang, D.B., Dadgar, J., Magrane, G., Dugaiczyk, A., Smitth, K.A., Cox, D.R., Masters, S.B. and Myers, R.M.

1 (base 2 to 435)

2 (base 2 to 435)

3 (base 2 to 435)

3 (base 2 to 435)

4 (base 2 to 435)

5 (base 2 to 435)

6 (base 2 to 435)

                                                                                                                                                  M95263.1 GI:177262
M95263.1 GI:177262
M95275; human chromosome 4; sequence tagged site.
Homo sapiens, clone C4-177 from Los Alamos National Laboratory chromosome 4 cosmid library, plate 4-1-2R, pos3C; vector Supercos
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                          HUM4STS161 435 bp DNA STS 26-FEB-1996
Human chromosome 4 sequence-tagged site STS4-161, sequence tagged
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University of California San Francisco
San Francisco, CA 9413-0925 USA
Phone: (415) 502-1612 Fax: (415) 476-8391
e-mail: hgmcprobes@cgl.ucsf.edu.
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Olivier,M. and Cox,D.R.
Unpublished, Olivier, M., Cox, D.R. (2000)
Unpublished (2000)
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92 TGTTGGAAGCTACCTTTTGATA 113
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AF644659 Caenorhabdi
U07562 Human ABL q
AC026482 Homo sapi
AC036482 Homo sapi
AC083757 Homo sapi
AC083757 Homo sapi
AC018618 Drosophil
AC01861 Drosophil
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AC018619 Homo sapi
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AC021315 Homo sapi
AC02578 Homo sapi
AC025378 Homo sapi
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1 (bases 1 to 239)
Jiang, G., McKenzie, T.L., Conrad, D.G. and Shechter, I.
Transcriptional regulation by lovastatin and 25-hydroxycholesterol in HepG2 cells and molecular cloning and expression of the CDNA for the human hepatic squalene synthase
J. Biol. Chem. 268 (17), 12818-12824 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-MAR-1998) Biochemistry and Molecular Biology, Uniformed Services University of the Health Sciences, 4301 Jones Bridge Road, Bethesda, MD 20814-4799, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5' end.
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Homo sapiens squalene synthase gene, intron 2,
AF051649.1 GI:4415976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 239)
Guan, G., Dai, P.H. and Shechter, I.
Direct Submission
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33. .>239
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VERSION KEYWORDS SEGMENT SOURCE

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FEATURES

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JOURNAL MEDLINE

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Location/Qualifiers
1. 1015
/organism="small round structured virus"
/isolate="patient; SRSV-CHIBA-407/87/J"
/db_xref="taxon:37141"
/note="SRSVs are currently recognised as a potential human calicivirus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MAQAIIGAIAASAAGSALCAGIQAGAEAALQAQRYQQDLTLQQN
SFNHDKEMLGYQMENSNKLLAKNLNTRYSLLQAGGLSSSDAARAVAGAPVTRLVDWGG
YRAAPQSSATTLRSGNFAWYDLPAQPKQKPLASEGYSNPAYDPVQRTASWVQSQNSS
RSWGPYHRQALQTVWYTPFGSTSSSYSTAPRGYFNTDRLPLFANLRR"
251 c 233 g 302 t
                                                                                                                                                                                                                                                                                                                                /translation="VPCLLPQEYITHFISEQAPIQGEAALLHYVDPDTNRNLGEFKLY
PGGYLTCVPNSSSTGPQQLPLDGVFVFASWVSRFYQLKPVGTAGPARGRLGVRR"
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Submitted (04-JUN-1998) Bigot Y., Institut de Recherche sur la
Biologie de l'Insects, UPRESA CNRS 6035, Facult des Sciences, Parc
Grandmont, 37200 Tours, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos.
1 (bases 1 to 1257)
Demattei, M.V., Auge-Gouillou, C., Pollet, N., Meunier-Rotival, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
   2 (bases 1 to 1015)
Utagawa,E.T., Takeda,N., Inouye,S., Kasuga,K. and Yamazaki,S.
3'-terminal sequence of a small round structured virus (SRSV) in
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Pred. No. 1.1e+03;
0; Mismatches 8; Indels
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94256839
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/db_xref="GI:1232113"
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/db_xref="G1:1232112"
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/db_xref="taxon:9913"
/clone="btmlec4"
263 c 263 g
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1 Similarity 63.6%;
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Direct Submission
Direct Submission
Direct Submission
T. Utagawa, National Institute of Health; 1-23-1 Toyama,
Shinjuku-ku, Tokyo 162, Japan (Tel:03-5285-1111(ex.2562),
Fax:03-5285-1177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAC ends sequenced at TIGR from the RPC111 BAC library. Designed and developed at the Stanford Human Genome Center. Location/Qualifiers
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Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
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94 degrees C for 30 sc
60 degrees C for 30 sc
72 degrees C for 23 sc
30
Perkin Elmer 9700
                                                                                                                                                                                                                                                                                                           25 ng
each 1 uM
each 200 uM
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small round structured virus
Viruses; ssRNA positive-strand viruses, no
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Pred. No. 1.2e+03;
0; Mismatches 8;
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                                   4005 Miranda Ave. 2nd Fl., Palo Altc
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@ehgc.stanford.edu
Primer A: GCACATTAGCTCTTGGATTGCTT
Primer B: TGCCTTGTGGTTTAGCATTTTT
STS SIZE: 278
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                    AmpliTaq Gold Polymerase:
Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="8"
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50 mM
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31. .308
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PCR Cycles:
Thermal Cycler:
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Best Local Similarity 63.6%;
Matches 14; Conservative
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Submitted (04-JUN-1998) Bigot Y., Institut de Recherche sur la
Biologie de 1'Insects, UPRESA CNRS 6035, Facult des Sciences, Parc
Grandmont, 37200 Tours, FRANCE
Location/Qualifiers
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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 Bigot, Y.
Direct Submission
Direct Submission
Submitted (04-JUN-1998) Bigot Y., Institut de Recherche sur la
Biologie de 1/Insects, UPRESA CNRS 6035, Facult des Sciences, Parc
Grandmont, 37200 Tours, FRANCE
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Bos taurus mariner related transposon Hsmarl, clone btmlec2.
AJ009223
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Pred. No. 1.1e+03;
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/db_xref="taxon:9913"
/clone="btmlec2"
a 261 c 248 g 3
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1. 1258
/organism="Bos taurus"
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/db_xref="taxon:9913"
/clone="btmlec3"
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transposon.
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Best Local Similarity 63.6%;
Matches 14; Conservative
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Bos taurus
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Demattei,M.V., Auge-Gouillou,C., Pollet,N., Meunier-Rotival,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (04-JUN-1998) Bigot Y., Institut de Recherche sur la
Submitted (04-JUN-1998) Bigot Y., Institut des Sciences, Parc
Biologie de 1'Insects, UPRESA CNRS 6035, Facult des Sciences, Parc
Grandmont, 37200 Tours, FRANCE
Location/Qualifiers
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1257)
Demattei, M.V., Auge-Gouillou, C., Pollet, N., Meunier-Rotival, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Features of the mammal marl transposons in the human, sheep, cow and mouse genomes and implications for their evolution Mamm. Genome In press 2 (bases 1 to 1258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peatures of the mammal marl transposons in the human, sheep, cow and mouse genomes and implications for their evolution Mamm. Genome In press 2 (bases 1 to 1257)
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Bos taurus mariner related transposon Hsmarl, clone btmlec3.
AJ009224
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Homo sapiens mariner related transposon Hsmarl, clone mlehsc3.
AJ009229
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Pred. No. 1.1e+03;
0; Mismatches 8; Indels
                                                                 63.6%; Score 14; DB 3; Length 12f
63.6%; Pred. No. 1.1e+03;
tive 0; Mismatches 8; Indels
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/transposon="Hsmarl"
/db_xref="taxon:9606"
/clone="mlehsc3"
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36 TGTTGGAATTTGCCATTTGATA 57
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Best Local Similarity 63.6%;
Matches 14; Conservative 0
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transposon.
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Best Local Similarity 63.6
Matches 14; Conservative
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Bos taurus
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source

FEATURES

JOURNAL AUTHORS

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BASE COUNT ORIGIN

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DEFINITION

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Submitted (12-JUN-1996) Microbiology, Monash University, Wellington Rd., Clayton, VIC 3168, Australia Location/Qualifiers
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LAVYKKATQVDQQQSK PFPI DFILDRVWVNSLSQI QFLKI A I QSDFFPPQNSTKKRI D
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Dictyostellum discoideum
Dictyostellum discoideum
Eukaryota; Dictyostellida; Dictyostellum.
1 (bases 1 to 2321)
Loomis,W.F.
Direct Submission
Submitsed (15-40G-1996) Dept. of Biology 0322, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="site of plasmid insertion in mutant organisms; mutants form crinkled, branching fingers; neither spores nor stalk cells were seen"
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Dictyostellum discoldeum ORF DG1040 gene, partial cds.
U66913
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/note="ORF DG1040; initially derived from a plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1481;
                                                                                                                                                                                                                                                                                                                                  2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14; DB 2;
Pred. No. 1.1e+03;
                                                                                                                                    /organism="Leptospira fainei"
/strain="Hurstbridge"
/db_xref="taxon:48782"
<1. ...>1481
/product="16S ribosomal RNA"
a 335 c 439 g 314 t
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/cell_line="AX4"
join(370. .732,813. .>2321)
/note="ORF DG1040"
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/db_xref="GI:1519538"
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Best Local Similarity 63.6%;
Matches 14; Conservative
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DDU66913/c
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VERSION
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AUTHORS
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YDNRRRPAQWLDREEAPKHFPKPNLHQKKVMYTVWWSAAGLIHYSFLNPGETITSEKY
AQOIDEMHRKLQRLQPALVNRKGPILLHDNARHVAQPTLQKLNELGYEVLPHPPYSP
DLSPTDYHFFKHLDNFLQGKRPHNQQDAENAFQEFVESRSTDFYATGINKLISRWQKC
VDCNGSYPD"
1256. .1287
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VQWWFKKFCKGDESLEDEERSGRPSEVDNDQLRAIIEADPLTTTREVAEELNVDHSTV
                                                                                                                                                                   Moderate and European Moderation of the Name of the Na
                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases i to 1481)

Perolat.P., Chappel.R.J., Adler.B., Baranton,G., Bulach,D.M., Billinghurst,M.L., Letocart,M., Merien,F. and Serrano,M.S. Leptospira fainel sp. nov., isolated from pigs in Australia lnt. J. Syst. Bacteriol. 48 Pt 3, 851-858 (1998)
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Adler,B., Chappel,R.J., Baranton,G., Bulach,D.M.,
Billinghurst,M.L., Letocart,M., Merlen,F., Serrano,M.S. and
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Leptospira fainei 16S ribosomal RNA gene, partial sequence.
U60594
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Pred. No. 1.1e+03;
0; Mismatches 8;
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/protein_id="AAC52010.1"
/db_xref="GI:1263081"
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/db_xref="taxon:9606"
/transposon="Hsmarl"
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284 c 278 g
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179. .1210
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63.6%;
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Leptospira fainei
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les 14; Conservative
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AIANRRALIKSQLETTTSDFDREKLQERLAKLAGGVAAKTTVDKOSTVIVEGSGSSE
ALNATRAAVEEGIVAGGGTALITVIEKVAALELEGDDATGRVIVEALEEEVRQIALN
TGYGSVVVIVDEKKNSPAGTGFNAATGEWVDMIKTGIIDPVKVTRSALQNAASLIL
TTEAVVANKPEPAAPAPAMPAGMDPGMMGGF"
1509. .1564
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KKVSNIQDILPLLEEVLKTNRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFG
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/translation="DHFENMGAKLVSEVASKTNDIAGDGTTTATVLTQAIVHEGLKNV
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Submitted (29-JUN-1995) A. Podbielski, Institut f Med
Mikrobiologie, an der Rhein Westf. Techn. Hochschule, Aachen,
Pauwelsstr Klinkum, 52057 Aachen, FRG
                                                              Gaps
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groEL gene; heat shock protein 60 (GroEL) like protein.
Streptococcus pyogenes.
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Pred. No. 1e+03;
0; Mismatches 8; Indels (
                               Length 2321;
                          Score 14; DB 32; Length 23
Pred. No. 1.1e+03;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Related Sequences M81132, M84965.
Location/Qualifiers
1. 2683
/organism="Streptococcus pyogenes"
/strain="serotype M49"
/isolate="CS101"
                                                                                                                                                                                                        BCT
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Pohl, B., Podbielski, A. and Zarges, I.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA61520.1"
/db_xref="G1:2462692"
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                                                                                                                                                                                           S.PYOGENGN 2683 bp DNA S.PYOGENES DNA for groEL gene.
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2069 TGTTGGATATAATTCTTTGATA 2048
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                            Query Match 63.6%;
Best Local Similarity 63.6%;
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1 (bases 1 to 2683)
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/procein_id="Caao2849.1"
/db_xref="GI:2300194"
/db_xref="GI:2300194"
/translation="AQVNDYNKISGYAKEAVQALVDQGVIQGDTNGNFNPLNTVTRAQ
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EAAKILIVEAFGLEGEABLSEFRDASQVKPWAKKYLEIAVANGIFEGTDANKLNPNNSI
TRQDFALVFKRTVDKVEGETPEEAAFVKAINNTTVEVVTFEEEVTNVQALNFKIEGLEI
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KLGQEVKVQAKVTVAEGQSKAGIPVTFTVPGNNNDGVVPTLTGEALTNEEGIATYSYT
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PKTGKPEANKTFNVGFVENMNVTSDKVANATVNGVKALQLSNGTALDAAQITTDSKGE
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     07-MAR-1997
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       PAT
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Deblaere,R.Y., Desomer,J. and Dhaese,P.
EXPRESSION OF SURFACE LAYER PROTEINS
PATENT: WO 9519371-A 14 20-JUL-1995;
SOLVAY (BE)
                                                                                                                                                                                        1 (bases 1 to 3666)
Deblacre,R.Y., Desomer,J. and Dhaese,P.
EXPRESSION OF SURFACE LAYER PROTEINS
PATENT: WO 9519371-A 13 20-JUL-1995;
SOLVAY (BE)
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Sequence 14 from Patent W09519371.
A45820
A45820.1 GI:2300193
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A45819 3666 bp DNA
Sequence 13 from Patent W09519371.
A45819
A45819.1 GI:2300192
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/organism="unidentified"
/db_xref="taxon:32644"
a 662 c 676 g 104
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ADYTRATGEGFTLNIDNAGAQVINLAGKKGAQGVADAINATFAGTATVSGDKVVIKSA
TTGVGSEVETYFSSVNQVUNAVVNGKDQVVAGTAATKAFTITTALSVGEKVVIDGVEY
TTAVAEGTAPTANTFVSSAANTLASVADQAANLAATIDTLNTADKFTASATGATITT
STVTPVGTTITEPVITLK"
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MMLSNWALSPRYVGQRNLIHCTTLFHTLTRWAKDADDKYHDINSMYENMFTPSNDNVS
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IQSLSTSPYYNLALENYVFKNTPRAKRGPDNCRLLFYINDRCAVIGKNONLWQEVDLA
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SSGVHSVKSKIKNVGIITPNQFIAVVSERFQKTFKVDGEIPIYYCDEFKSINDEIKDA
MNTLQSEQWKYFSGPKFSVKIKDKGLTIKVEKGMIYDCDRNDLIGLEFKGFLENIDSY
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetacees; Saccharomyces.

1 (bases 1 to 3915)
Pohl, T.M. and Aljinovic, G.
Unpublished
2 (bases 1 to 3915)
MIPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submission Submitted (25-SEP-1995) Data collected by MIPS on behalf of the Submitted (25-SEP-1995) Data collected by MIPS on behalf of the European yeast chromosome X sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG, E-mail: Mewes@mips.embnet.org
                                                                                                                                                                                                                                                    Gaps
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complement(2756. 3067)
/note="solo delta"
3266. 3337
/gene="tR(TCT)JL2 - systematic name"
3266. 3337
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                                                                                                                                                                                           Score 14; DB 81; Length 3666;
Pred. No. 1e+03;
0; Mismatches 8; Indels (
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S.cerevisiae chromosome X reading frame ORF YJL046w.
249321 X13136
249321.1 GI:1008176
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152. .1507
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complement(2445. .2735)
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/db_xref="SWISS-PROT:P47051"
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Best Local Similarity 63.6
Matches 14; Conservative
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/gene="tR(TCT)JL2 - systematic name"
3348. .3419
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/note="tRNA-Asp - common name; anticodon gene: GTC"
3348. .3419
/gene="tD(GTC)JL2 - systematic name"
a 667 c 698 g 1292 t
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Pred. No. 1e+03;
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X35887
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V25036
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                   Leptospira sp.
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L. fainei nucleoti
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Nucleic acid seque
                                                                   March 27, 2001, 08:22:59 ; Search time 207.51 Seconds
(without alignments)
39.827 Million cell updates/sec.
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                   480022 segs, 187831343 residues
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                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Claim 15; Page 72; 94pp; English.

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            This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainel. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and
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This sequence represents a Leptospira DNA sequence isolated from the pathogonic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainel. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and
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Mismatches
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Matches 22; Conserv
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Score 14; DB 19; Pred. No. 33; 0; Mismatches 8

63.6%; ilarity 63.6%; Conservative

Query Match Best Local Similarity Matches 14; Conserv

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Mizzen L, Wisniewski J;
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P-PSDB; Y23904.
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                                     06-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999
     17-SEP-1998
                                                                                                                                                 Chappel RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X86155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X86155/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                         of Ureaplasma urealyticum infection. It provides novel genes (x99501-681) that can be used as a source of primers and probes for the detection and or quantification of U. urealyticum in a biological sample. The probes that can be used in the method of the invention by forming target: probe complex is copmolementary to a region selected from one of the 181 nucleic acid sequences (x99501-681). U. urealyticum is an opportunistic pathogen of the human urogenital tract that is a significant cause of the human urogenital tract that is a significant cause of the infections are commonly asymptomatic, it is important to have specific and sensitive methods for detecting their presence in a patient. Also, as the pathogen has no current antibiotic directed specifically against it, it would be advantageous to isolate and detect gene sequences which are unique to it, and utilise these as a basis for diagnosis of urealyticum infection as well as to develop new and improved drug
                                                                                                                                                                                                                                                                                                                                                                                                                              present invention provides methods for the detection and diagnosis
Ureaplasma urealyticum; nucleic acid detection; infection; pathogen; human urogenital tract; pregnancy; neonatal disease; drug therapy; suppurative arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapies. The present invention provides such novel polynucleotide
                                                                                                                                                                                                                                                                                                                                              Detection of Ureaplasma urealyticum using novel genes, probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infection; pathogenic Leptospira; protective immunity; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20; Length 972;
53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                               Heiner CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 972 BP; 309 A; 127 C; 98 G; 438 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8;
                                                                                                                                                                                                                                                               Glass JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.6%; Score 14; DB
llarity 63.6%; Pred. No. 53;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                               Glass JI,
                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 82; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L. fainei nucleotide sequence.
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                                                                 Ureaplasma urealyticum
                                                                                                                                                                                                                                (UABR-) UAB RES FOUND.
                                                                                                                                                                                                                                                               Chen EY,
                                                                                                                                                                                                                                                                                                              WPI; 1999-469343/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leptospira fainei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9840099-A1.
                                                                                                  WO9939007-A1
                                                                                                                                                                                                30-JAN-1998;
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                                                                                                                                                                                                                                                                              Lefkowitz E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JAN-1999
                                                                                                                                  05-AUG-1999
                                                                                                                                                                                                                                                               Cassell GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                 primers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainei. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for prophylactic or detection and diagnosis of past or present LS infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a Leptospira DNA sequence isolated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat shock protein; Hsp60-2; immune response; immunological carrier; cancer control; tumour; sarcoma; cancer; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding heat shock protein-60 from Streptococcus, useful in vaccines, as carriers for other immunogens, as anticancer agents and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding a Streptococcus pyogenes heat shock protein (Hsp)60-2.
                                                                                                                                                                                                                                                                                                                                                                              New isolated pathogenic Leptospira bacterium - useful for, e.g developing products for conferring protective immunity, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Length 1477;
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Pred. No. 56;
0; Mismatches
                                                                                                                           (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
(PIGR-) PIG RES & DEV CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                               developing products for conferring proprophylactic or therapeutic treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 69-70; 94pp; English.
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Local Similarity 63.6%;
les 14; Conservative
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98WO-AU00145
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                                                             97AU-0005494
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Disclosure; Fig.6; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia chafeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-254290/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection; dog; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ehrlichia canis
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                                                                                                                                                                                                                                                                                                                                                      X34752;
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X \times C C C C C \times S
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                                                                                                                                                                                                                                                                                                                                       0;
                                 The present sequence encodes a heat shock protein, designated Hsp60-2. The protein, its fragments, variants and fusion proteins, are used to elicit or enhance an immune response against Streptococcus, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, overy, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Host cell expressing surface layer protein fusion protein - used for host presentation of antigens and vaccine prodn.
                                                                                                                                                                                                    of the protein, as a source of primers and probes for detecting streptococci in standard hybridization/amplification assays, and
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Surface layer protein; SLP; fusion protein; vaccine; antigen; surface expression; epitope; ds.
                                                                                                                                                                                                                                                                                                         Length 1661;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                             Sequence 1661 BP; 512 A; 308 C; 407 G; 434 T; 0 other;
                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                              therapeutically in gene therapy vectors.
                                                                                                                                                                                                                                                                                                         Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
       Claim 3; Fig 4A-B; 176pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                1163 TGTTGGAGCTCCTACTTGATA 1142
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                                                                                                                                                                                                                                                                                                        63.6%;
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/*tag= a
95..3853
/*tag= b
95..184
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185..3850
                                                                                                                                                                                                                                                                                                                                    14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B. sphaericus SLP gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus sphaericus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-263827/34.
P-PSDB; R80530.
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SOLV ) SOLVAY SA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 099430
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
Q99430/c
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Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in Y06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in Y06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
A probe based on the N-terminal sequence of B. sphaericus P-1 (LMG 9-13855) surface layer protein was used to screen an HindIII-generated library to isolate the slp gene. Promoter regions of the gene are used in genetic constructs providing surface expression of heterologous proteins in P-1 hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides isolated outer membrane proteins (OMP) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
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                                                                                                                                                                                                                                                                           DB 16; Length 4197;
63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 59.1%; Score 13; DB 20; Length 396; Best Local Similarity 61.9%; Pred. No. 1.7e+02; Matches 13; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                              Sequence 4197 BP; 1470 A; 731 C; 763 G; 1233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 396 BP; 147 A; 49 C; 58 G; 142 T; 0 other;
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                        Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 12A; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                2836 TGTTGGAGCAACTGGTTTGATA 2815
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                                                                                                                                                                                                                                                                                                                                                                                           1 tgttggannnnnnntttgata 22
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                                                                                                                                                                                                                                                                        63.6%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding OMP-1T protein.
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                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 65...
Local 14; Conservative
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The present invention describes a library of human polynucleotides comprising the sequences given in 21552 to 21779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in 21253 to 21779. The polynucleotides can be used as a source of primers and probes, which be used for a variety of purpose, e.g. detection of expression levels, mapphing, tissue typing or profilling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrangements (wind succeed protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify a succeed protein); and to detect the invarience of an encoded protein); and to detect the invarience of an encoded protein); and to detect the invarience of an encoded protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer). The polynuclectides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                                           Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                     Human gene expression product cDNA sequence SEQ ID NO:4205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escobedo J, García PD, García V, Glese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard
Stache-Crain B, Sudduth-Kiinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 828 BP; 189 A; 155 C; 172 G; 227 T; 85 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1992; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide analogues and antagonists.
                                        216735 standard; cDNA; 828 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0080666.
98US-0072910.
98US-0075954.
                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US01619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0080114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0080515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crkvenjakov R, Dickson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-494092/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                            WO9938972-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-1998;
03-APR-1998;
                                                                                                                          12-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-1998;
24-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                       05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-APR-1998
                                                                                z16735;
6
RESULT
                        216735
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Hydronephrosis gene; HNG gene; USF2 gene; renal disease; renal aplasia; vesical-ureteral reflux; pelvi-ureteral junction obstruction; multicystic renal dysplasia; renal agenesis; hydronephrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detectidiseases related to Borrelia infections in animals, and for the .
                                                                                                                                                                                                                     Treponema pallidum infection; syphilis; Borrelia infection; animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                      Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.1%; Score 13; DB 20; Length 1079; 61.9%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of breakpoint region on chromosome 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1079 BP; 397 A; 280 C; 181 G; 221 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  production of biosynthetic products such as enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 842-843; 1150pp; English.
               199 tgttggagaattcattttgnta 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1022 GTTGGATTAAGGTGTTTGATA 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ő
22
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                                                                                                  X20676 standard; DNA; 1079 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                      98WO-US13041.
                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
1 tgttggannnnnnntttgata
                                                                                                                                                                                                                                                                                                                                                                                  97US-0050667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V18099 standard; DNA; 1482
                                                                                                                                                         05-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-081273/07.
                                                                                                                                                                                                                                     enzyme production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                               Treponema pallidum
                                                                                                                                                                                                                                                                                          WO9859034-A2.
                                                                                                                                                                                                                                                                                                                                                     23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1997;
                                                                                                                                                                                                                                                                                                                         30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser CM;
                                                                                                                              X20676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V18099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
V18099
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                                                                                   x20676/c
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Gaps

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Length 828;

Score 13; DB 20; Length 82 Pred. No. 1.8e+02; 0; Mismatches 9; Indels

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59.1%; 59.1%;

Query Match 59.1 Best Local Similarity 59.1 Matches 13; Conservative

Mitogen activated protein kinase; MAP; infectious specific protein; plant; jasmone acid; ss.

JP09065881-A.

Synthetic.

11-MAR-1997

MAP kinase #2 coding sequence.

04-JUN-1997

T60350;

T60350 standard; cDNA to mRNA; 1786 BP.

268 tgttggattttcctctttgat 288

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RESULT 12
                                                 T60350/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reflux, uni or bilateral pelvi-ureteral junction obstruction, multicystic renal dysplasia, renal agenesis, renal aplasia, hydronephrosis, von Mayer-Rokitansky-Kuester disorder and bifid ureter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This represents the nucleotide sequence of the breakpoint region on der(19) which reveals that the transcriptional orientation of the hydronephrosis (HNG) gene on the short arm of chromosome 6 is from the telomere to the centromere. A translocation partner to this gene on chromosome 6 is the chromosome 19 USF2 gene. The HNG gene can be used as a starting point to design suitable compounds or techniques for the diagnosing cells involved in renal diseases or disorders, or nucleotide probes for diagnosing cells involved in renal diseases and disorders. A protein or preparing suitable antibodies for diagnosing cells involved in renal diseases and disorders. The products and method can be used to treat or diagnose renal diseases and disorders and method can be used to treat or diagnose renal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydronephrosis gene - useful to treat or diagnose renal diseases and disorders, e.g. vesical-ureteral reflux, pelvi-ureteral junction obstruction, multicystic renal dysplasia or renal agenesis
                                                                                                                                                                                                                                                                                   "partial sequence of exon 7 of USF2 gene;
the transcriptional orientation is from the
                                                                      /*tag= a
/note= "sequences derived from chromosome 6p21."
                                                                                                                                                                                                                         /*tag= e
/note= "chromosome 19-derived USF2 sequences"
1466..1477
                                                                                                                   'note = "partial intronic sequence of HNG
Von Mayer-Rokitansky-Kuester disorder; bifid ureter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1482 BP; 423 A; 310 C; 288.G; 460 T; 1 other;
                                                                                                                                                                                                                                                                                                            centromere to the telomere"
                                                                                                                                                                                                                                                                                                                                                                                                                           (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van De Ven WJM;
                                                                                                                                                                 "exon 9 of HNG
                                                                                                                                                                                        /*tag= d
/note= "Alu repeats"
                                             Location/Qualifiers
1..1222
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 9-3; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                               97WO-EP05583
                                                                                                                                                                                                                                                            /*tag= f
/number= 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fryns JPGJ, Groenen PMA,
                                                                                                                                                      'number= 9
                                                                                                                                                                                                             223..1482
                                                                                               1..22
/*tag= b
                                                                                                                                            O
                                                                                                                                                                  /note= "e:
356..533
                                                                                                                             23..170
                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-240833/21.
                         Homo sapiens
                                                         misc_feature
                                                                                                                                                                             misc_feature
                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                WO9815650-A2
                                                                                                                                                                                                                                                                                                                                                                              09-OCT-1997;
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                                                                                             intron
                                                                                                                               exon
                                                                                                                                                                                                                                                  exon
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                                                                                                                                                                                                                                                                                                                                                                                           T60349 and T60350 represent the coding sequences for the mitogen activated protein (MAP) kinases of the invention. The protein encoded by this sequence contains the T-E-Y sequence, in which the threonine and tyrosine residues are phosphorylated to activate the protein at residues 249-231. The MAP kinase and its gene can be used to regulate the synthesis of jasmone acid and the synthesis of a group of infectious synthesis of jasmone acid and the mAP kinase gene into a plant, thereby inducing expression of the mRNA for MAP kinase (or its antisense PNNA), the synthesis of jasmone acid and a group of infectious specific proteins can be regulated in the plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virulence, P7C18; vaccine; antibacterial; antibiotic; screening; phosphoribosylformylglycinamide decarboxylase; PurL; ss.
                                                                                                                                                                                                                                  Wound-stress inducible MAP kinase - used to regulate the synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.1%; Score 13; DB 18; Length 1786; 61.9%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1786 BP; 503 A; 390 C; 353 G; 540 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus mutant P15C31 virulence gene.
                                                              (NORQ ) NORINSUISANSHO NOGYO SEIBUTSU SHIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                Disclosure; Page 14-16; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13 .
X07102
ID X07102 standard; DNA; 2190 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 tgttggannnnnnntttgat 21
95JP-0220935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 TGTTGGATATTTTTATTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAY-1999 (first entry)
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus.
                                                                                                                                WPI; 1997-220416/20.
P-PSDB; W15513.
                                                                                                                                                                                                                                                                        of jasmone acid
29-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Gaps

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59.1%; Score 13; DB 19; Length 1482; larity 61.9%; Pred. No. 2e+02; Conservative 0; Mismatches 8; Indels

Local Similarity tes 13; Conserva

Matches

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Query Match

1 tgttggannnnnnntttgat 21

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somitogenesis zebrafish cDNA libraries with a probe corresponding to the Drosophila melanogaster FTZ-Flalpha DNA binding domain. The isolated clones can be used to produce RNR delta and espsilon polypeptides useful for modifying retinoid activity and identifying specific target genes implicated in retinoid responses important in
                                                                                                                                                                                                                                            Isolated retinoid X receptor protein - having amino acid insert in ligand binding domain, useful to identify specific target genes implicated in retinoid responses important in disease states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRBAP-1; carbohydrate-associated protein 1; human; autoimmune disorder; inflammathon; gastrointestinal disorder; infection; reproductive disorder; neurological disorder; eye disorder; cell proliferation; cancer; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "a polynucleotide containing C at position 428 is specifically claimed in Claimed 21"
                                                                                                                                                                                                                                                                                                                                                            cDNA clones (T67196 and T67197) respectively code for novel retinoid X receptors RXR delta (W18032) and RXR epsilon (W18033) that exhibit a high degree of amino acid conservation with other vertebrate RXRs but which represent unique subtypes defined by an additional 14-amino acid segment in their ligand binding domains. The RXR epsilon clone was isolated by screening adult and post-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13; DB 18; Length 2508; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2508 BP; 600 A; 652 C; 646 G; 610 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human carbohydrate-associated protein CRBAP-1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            Claim 8; Page 29-30; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/frequency= "0.10"
                                                                                                                                            Petkovich M;
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                                                                                                   (TOOH ) UNIV QUEENS KINGSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.1%;
61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294941/c
ID 294941 standard; cDNA; 3519
                   96CA-2177642.
                                                          95US-0462182.
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Best Local Similarity 61.90
****hes 13; Conservative
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                                                                                                                                                                                  WPI; 1997-298660/28
                                                                                                                                            Ohno C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200018922-A2.
                                                                                                                                                                                                        P-PSDB; W18033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                   29-MAY-1996;
                                                          05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2000
                                                                                                                                            B,
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                                                                                                                                            Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                       This is the nucleotide sequence of a virulence gene identified in Staphylococcus aureus mutant P15C11. S. aureus genes (see X07088-136) associated with virulence were identified by signature-tagged mutants containing a chromosomal insertion of a signature tagged transposon were generated, mutants with attenuated virulence were identified in amouse model of bacteraenia, attenuated virulence were identified in amouse model of bacteraenia, and the nucleotide sequences of the regions flanking the transposon insertion sites of these mutants were determined. Database sequence comparisons were performed to identify the virulence genes and to determine the possible function of their protein products (see also W97680-724). The P15C31 virulence gene product (see W97694) was identified as phosphoribosylformylgycinamic decarboxylasse Purt, an enzyme involved in purine biosynthesis. A claimed method of identifying an antibacterial agent involves assaying potential agents for the ability to interfere with the expression of S. aureus containing a functional mutation in one of the virulence genes, and its use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                            - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20; Length 2190;
                                                                                                                                                                                                                                                                                                                          Inhibition of virulence genes from Staphylococcus aureus for, e.g. screening for potential anti-microbial agents
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Pred. No. 2.1e+02;
0; Mismatches 8;
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                                                                                                                                                                              (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 86-89; 203pp; English.
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Best Local Similarity 61.9%;
Matches 13; Conservative (
                                                                                                98WO-GB01974.
                                                                                                                                       97US-0887534
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                 W09901473-A2
                                                                                              03-JUL-1998;
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RESULT 14

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The present sequence is that of cDNA coding for a novel human carbohydrate-associated protein, termed CRBAP-1 (see Y7956).

The cDNA (Incyte clone 714029) was initially identified in prostate tumour cDNA library PROSTUTO1. The sequence contains a single nucleotide polymorphism with C replacing T at position cases and at position 428 in 10% of the clones, and to 428 in 10% of the clones, and the case of the action of the clones and cell in 10% of clones. CRBAP-1 resembles vertebrate galactoside-binding vas identified in libraries associated with cancer and cell proliferation, inflammation and immune response, reproductive tissues and nervous tissues. The invention provides CRBAP-1 to -7 polymorbotides (see 294941-48) and polypeptides (see Y19505-11), as well as expression vectors, host cells, antibodies, agonists and antagonists. These are used in the diagnosis, treatment or prevention of disporders associated with CRBAP expression.

Sepecially autoimmune or inflammatory disorders, gastrointestinal clisorders, infectious disorders, reproductive disorders, and sorders, including cancer. CRBAP polynucleotides are useful sample from a patient. They may also be administered as part of
                                                                                                                                                                                                                                                                                                                      Novel carbohydrate-associated proteins used for the prevention and treatment of autoimmune/inflammatory disorders of e.g. the gastrointestinal and reproductive systems -
                                                                                                                                                                                                         Au-Young J, Lal P, Bandman O, Reddy R, Baughn MR, Yue H;
Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3519 BP; 1067 A; 627 C; 730 G; 1095 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 90-91; 104pp; English.
                                                                        98US-0167179.
98US-0191838.
98US-0205656.
98US-2223333.
                      99WO-US22685
                                                          98US-0164785
                                                                                                                                                                       (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                  WPI; 2000-317516/27.
P-PSDB; Y79505.
                                                    01-OCT-1998;
06-OCT-1998;
13-NOV-1998;
03-DEC-1998;
03-DEC-1998;
                  29-SEP-1999;
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Gaps 0; Ouery Match Best Local Similarity 61.9%; Pred. No. 2.2e+02; Matches 13; Conservative 0; Mismatches 8; Indels (

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1909 TGTTGGAGTCACCTGTTTGAT 1889

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Search completed: March 27, 2001, 08:23:01 Job time: 5303 sec

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STRANDEDNESS:
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Best Local Simi
Matches 14;
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Sequence 3, A
Sequence 3, A
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Sequence 118
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-714-918-19
US-08-714-918-19
US-08-473-446-118
US-08-752-238-2
US-09-085-6038-2
US-09-031-897-6
US-08-752-238-1
US-08-752-238-1
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US-08-212-133A-5
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                                                  - nucleic search, using sw model
                                                                      March 27, 2001, 08:19:22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/08682517
; Batent No. 5874267
; GENERAL INFORMATION:
: TITLE OF INVENTION: Expression of surface layer proteins
: TITLE OF INVENTION: Expression of surface layer proteins
: TITLE OF INVENTION: Expression of surface layer proteins
: TITLE OF INVENTION: 25
: COMPUTER READABLE FORM:
: COMPUTER: IBM PC compatible
: COMPUTER: IBM PC compatible
: COMPUTER: PatentIN SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIN NEGEOSE #1.0, Version #1.30 (EPO)
: APPLICATION NUMBER: US/08/682,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expression of surface layer proteins 25
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TITLE OF INVENTION: Expression of surface layer protein NUMBER OF SEQUENCES: 25
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,517
US-09-058-489-20
US-08-362-525-1
US-08-670-708-36
US-09-280-443-5
US-09-280-739-1
US-08-280-739-1
US-08-791-8458-1
US-08-791-8458-1
US-08-639-501-23
US-08-639-501-23
US-09-044-908-23
US-09-044-908-23
US-09-184-658-11
US-08-419-009-19
US-08-419-009-10
US-08-419-009-10
US-08-419-009-10
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2652 TGTTGGAGCAACTGGTTTGATA 2631
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                             6057
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,517
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STATE: California
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MOLECULE TYPE: DN
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                              NAME/KEY:
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US-08-682-517-8
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Mismatches 8; Indele
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25;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Thoppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PELIGIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,517
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Pred. No. 25;
0; Mismatches
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Pred. No.
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Patent No. 5874267
GENERAL INFORMATION:
APPLICANT:
     CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3666 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 63.6%;
Matches 14; Conservative
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63.68;
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 4197 base pairs
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NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy discompa
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EDNESS: single
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; LOCATION: 1..3
US-08-682-517-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CL. COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
"TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C.-DOS 5.0 SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: MOLECURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FTITING DATE: September 13, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
10S-08-714-918-19
Sequence 19, Application US/08714918
Patent No. 603/123
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APPLICATION NUMBER: 60/009,102
                                                                                                                                                                                ORGANISM: Bacillus sphaericus INDIVIDUAL ISOLATE: P-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2836 TGTTGGAGCAACTGGTTTGATA 2815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 tgttggannnnnnntttgata 22
                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.6%;
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 4197 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 63.6
Best Local Similarity 63.6
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                         mat_peptide
185..3850
                                                                                                                                                                                                                                                                                                                                                                sig_peptide
95..184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Benton, Bret
                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICANT: PACLETI, ENZO
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR
TITLE OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
         Gaps
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Pred. No. 1.7e+02;
0; Mismatches 9; Indels
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Patent No. 5804418
GENERAL INFORMATION:
APPLICANT: Lambowitz Dr., Alan M
APPLICANT: Mohr Dr., Georg
APPLICANT: Saldanha Dr., Roland
APPLICANT: Marsuura Dr., Manabu
TITLE OF INVENTION: Integrase
TITLE OF INVENTION: Integrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,446
         6
       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEW YORK
UNITED STATES OF AMERICA
                                                                                                                                                             RESULT 7
US-08-473-446-118
; Sequence 118, Application US/08473446
; Patent No. 6017542
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,118
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                                                                                              Db 1076 TGTTGGATAACTATTTTTATA 1097
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TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
                                                   1 tgttggannnnnnntttgata 22
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59.1%;
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Best Local Similarity 59.1
Matches 13; Conservative
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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       13;
         Matches
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APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR
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                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 5253;
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STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PLOPSY disk
COMPUTER: PLOPSY STATES
COMPUTER: PATENTINE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTINE RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                   59.1%; Score 13; DB 61.9%; Pred. No. 94; Live 0; Mismatches
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: FROMMEN, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 26,506
REFERENCE/DOCKET NUMBER: 26,506
REFERENCE/DOCKET NUMBER: 454310-2670
RELECHANTION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 1760 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/413,118 FILING DATE: 29-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 118, Application US/08413118 Patent No. 5688920 GENERAL INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/(TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                          LENGTH: 5253 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 61.9
Matches 13; Conservative
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                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-714-918-19
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Best Local Similarity
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| Sequence 6, Application US/09031897
| Sequence 6, Application US/09031897
| Patent No. 6027895
| GENERAL INFORMATION:
| APPLICANT: Lambowitz, Alan
| APPLICANT: Zimmerly, Steven
| APPLICANT: Zimmerly, Steven
| APPLICANT: Goorg
| APPLICANT: Wethods Cleaving DNA with Nucleotide
| TITLE OF INVENTION: Integrases
| TITLE OF INVENTION: Integrases
| VIMBER OF SEQUENCES: 12
| CORRESPONDENCE ADDRESS:
             PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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Pred. No. 1.7e+02;
                                                                        CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40.591
REFERENCE/DOCKET NUMBER: 24671/04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 22-8416
TELEPRATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: nucleic acid
"""""NUFEDESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.7e); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Calfee, Halter & Griswold
STREET: 800 Superior Avenue, Suite 1400
CITY: Cleveland
                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,603B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||||||
| 139 TATTGGAATATAAATTTTGATA 118
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: DOCHETLY, Pamela A.
REGISTRATION NUMBER: 40,591
REFERENCE/DOCKET NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION TELEPHONE: (216)542-8416
TELEPRAX: (216)241 0816
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 59.1
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION:
US-09-085-603B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Pred. No. 1.7e+02;
0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yang Dr., Jiam
APPLICANT: Tanger Dr., Jiam
APPLICANT: Zimmerly Dr., Steven
APPLICANT: Guo Dr., Huather
APPLICANT: Gall Dr., Clifford J.
TITLE OF INVENTION: Methods of Making an Rnp Particle
TITLE OF INVENTION: Having Nucleotide Integrase Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALFEE, HALTER & GRISWOLD LLP
                                      ADDRESSEE: CALFEE, HALTER & GRISWOLD STREET: 800 Superior Avenue CITY: Cleveland STATE: Ohio COUNTRY: US
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/752,238
                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lambowitz Dr., Alan M
APPLICANT: Mohr Dr., Georg
APPLICANT: Saldanha Dr., Roland
APPLICANT: Matsuura Dr., Manabu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09085603B Patent No. 6001608 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLITCK, MARY E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 2467:
TELECOMMUNICATION INFORMATION:
TELEFRORE: (216) 22-8458
TELEFRORE: (216) 24-0816
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 TATTGGAATATAAATTTTGATA 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 59.1%;
Matches 13; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1800 base pairs
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                FILING DATE
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                                                                                                                                                   ZIP: 44114
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; LOCATION:
US-08-752-238-2
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Gaps

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LENGTH:
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STATE:
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                                                                                                                                                                                  Length 1800;
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                                                                                                                                                                                                                        Indels
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ZIP: 75270-2197

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATORIIN PC-DOS/MS-DOS
SOFTWARE: PATORIIN DATA:
APPLICATION NUMBER: US/08/339,129
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08339129
Patent No. 5750399
GENERAL INPORMATION:
APPLICANT: Dixon, Richard A.
APPLICANT: Dalva, Nancy L.
APPLICANT: Commen, Abraham
TITLE OF INVENTION: Isoflavone Reductase Promoter NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                Score 12.4; DB 3;
Pred. No. 1.7e+02;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Richards, Medlock & Andrews
1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hansen, Eugenia S.
RECISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: NOBF B35969
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4600
TELEFAX: 214-939-4600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-752-238-1/c
; Sequence 1, Application US/08752238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        950 TGTTGGATTTCCTGCTTTAATA 929
                                                                                                                                                                                                                                                                                                    139 TATTGGAATATAAATTTTGATA 118
                                                                                                                                                                                                                                                               1 tgttggannnnnnntttgata 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 tgttggannnnnnntttgata 22
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic)
US-08-339-129-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                Query Match
Best Local Similarity 59.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2730 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                   1..1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 13; Conserv
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                                                                              ; NAME/KEY: CDS
; LOCATION: 1..1
US-09-031-897-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Dallas
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
STREET: 12
                                                                                                                                                                                                                                                                                                                                                                                 US-08-339-129-1/c
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Gaps
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APPLICANT: Guo Dr., Huatao
APPLICANT: Beall Dr., Clifford J.
TITLE OF INVENTION: Methods of Making an Rnp Particle
TITLE OF INVENTION: Having Nucleotide Integrase Activity
CORRESPONDENCE ADDRESS:
ADDRESSEE: CALFEE, HALTER & GRISWOLD LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                   APPLICANT: Mohr Dr., Georg
APPLICANT: Saldanha Dr., Roland
APPLICANT: Saldanha Dr., Manabu
TITLE OF INVENTION: Method for Preparing Nucleotide
TITLE OF INVENTION: Integrase
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: CALFEE, HALTER & GRISWOLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,238
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 800 Superior Avenue STREET: STREET S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CALFEE, HALTER & GRISWOLD STREET: 800 Superior Avenue CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 24671/00103 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lambowitz Dr., Alan M
Mohr Dr., Georg
Saldanha Dr., Roland
Matsuura Dr., Manabu
Yang Dr., Jiam
Zimmerly Dr., Steven
Guo Dr., Huatao
                                        Lambowitz Dr., Alan M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-085-603B-1/c; Sequence 1, Application US/09085603B Patent No. 6001608; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           890 TATTGGAATATAAATTTTGATA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: GOLITICK, MATY E.
REGISTRATION NUMBER: 34,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 tgttggannnnnnntttgata 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
Matches 13; Conserva
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INFORMATION:
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US-08-752-238-1
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
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LENGTH: 2761 base pairs
                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                       TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                      US-09-031-897-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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APPLICANT: Lambowitz, Alan
APPLICANT: Lambowitz, Alan
APPLICANT: Jamen's Georg
APPLICANT: Glow-rly, Steven
APPLICANT: Glow-rly, Steven
TITLE OF INVENTION: Methods Cleaving DNA with Nucleotide
TITLE OF INVENTION: Integrases
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & Griswold
STREET: 800 Superior Avenue, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTKI:

ZIP: 44114
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPETWARE: Patentin Release #1.0, Version #1.30
"C'N9/031,897
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,603B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.4; DB 3;
Pred. No. 1.8e+02;
0; Mismatches 9;
                                                                                                                                                                     CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: DOCNERTY, Famela A.
REGISTRATION NUMBER: 40,591
REFERENCE/DOCKET NUMBER: 24671/04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8416
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2761 base pairs
ILNGTH: 2761 base pairs
STRANDEDNESS: double
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: DOCLOGY: linear
MOLECULE TYPE: DNA (Genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40,591
REFERENCE/DOCKET NUMBER: 24671/00105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216)622-8416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09031897
Patent No. 6027895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 890 TATTGGAATATAAATTTTGATA 869
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Best Local Similarity 59.1%;
Matches 13; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Clevel
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-031-897-5/c
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Gaps
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                                                                                                                       Length 2761;
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schryvers, Anthony B
APPLICANT: Schryvers, Robin E
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yan, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
CORRESPONDENCE ADDRESS:
                                                                                                Score 12.4; DB 3; Length 2
Pred. No. 1.8e+02;
9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/613,009A FILING DATE: .08-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.4; DB 3;
Pred. No. 1.9e+02;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Palace
                                                                                                                                                                                                                                                                                                                    US-08-613-009A-1/c
; Sequence 1, Application US/08613009A
; Patent No. 6090576
                                                                                                                                                                                                                                        890 TATTGGAATATAAATTTTGATA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                 1 tgttggannnnnnntttgata 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 TGTTGGCTTTTGCACTTTGATA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 tgttggannnnnnntttgata 22
            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                     56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.4%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                 Query Match
Best Local Similarity 59.18
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Myers, Lisa E APPLICANT: Schryvers, Ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3438 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 59.1
Matches 13; Conservative
double
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STRANDEDNESS: single
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Search completed: March 27, 2001, 08:19:23 Job time: 5150 sec

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gb_est71:*
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em_esthum21:*
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em_esthum11:*
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em_esthum15:*
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em_esthum16:*
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em_esthum19:*
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gb_est41:*
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em_estind:*
em_estov1:*
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em_estpl1:*
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em_estom2:*
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em_estpl4:*
em_estpl5:*
em_estrol5:*
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em_estro11:*
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gb_est55:*
gb_est56:*
gb_est57:*
gb_est67:*
gb_est67:*
gb_est68:*
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em_estro4:*
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em_estro8:*
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9b_est48:*
9b_est49:*
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gb_est45:7
gb_est46:7
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                                                                                                                            March 27, 2001, 07:38:23 ; Search time 2517.78 Seconds (without alignments) 61.230 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                 7991742 seqs, 3503743858 residues
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Maximum Match 100%
Listing first 45 summaries
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17: em_est, 18: em_est, 19: em_est, 20: em_est, 21: em_est, 22: em_est, 23: em_est, 24: em_est, 25: em_est, 26: gb_est, 27: gb_est, 28: g	2. gb_est(6) 4. gb_est(6) 4. gb_est(6) 4. gb_est(7) 6. gb_est(7) 6. gb_est(7) 6. gb_est(7) 6. gb_est(8) 6. gb	158: 90-9850:: 159: 90-9850:: 160: 90-9850:: 161: 90-98510:: 162: 90-98510:: 163: 90-98510:: 164: 90-98512:: 165: 90-98512:: 165: 90-98512:: 167: 90-98512:: 168: 90-98512:: 170: 90-98512:: 170: 90-98512:: 171: 90-98513:: 173: 90-98521:: 174: 90-98521:: 175: 90-98521:: 176: 90-98521:: 177: 90-98521:: 177: 90-98521:: 177: 90-98521:: 177: 90-98521:: 178: 90-98521:: 179: 90-98521:: 177: 90-98521:: 176: 90-98521:: 177: 90-98521:: 178: 90-98521:: 178: 90-98521:: 178: 90-98521:: 178: 90-98521:: 178: 90-98521:: 178: 90-98521:: 178: 90-98521:: 178: 90-98521:: 178: 90-98521:: 178: 90-98521:: 178: 90-98521:: 179: 90-98521:: 179: 90-98521:: 177: 90-98521:: 177: 90-98521:: 178: 90-98521:: 1	em_gss1/ em_gss18

by chance to have a the result being printed,	ion.	BB357781 BB357781 BE059640 sp35a01	6 UI-M-BH	uc46f10.	1 BB28790	BE202756 EST402778	3 RPCI-23- AV546877	ST76G08	7 CITBI-E1 2 HS_3029_	6 an37g11 ug35b10	ab37h10.r	R89220 yp99a12.rl AW624588 EST322533	7 HS_3197	1882903.8 0 RPCI-11	mt25a11.x	9 KPCI-23 9 ux29e12	MtBA38F11	mc31D03.	10732 Lam	ug71a09.	ut80g10	vu09103.F HS 2136	BE353412 EST353789	EST43182	uo37a12.	EST32715	HS_5415	AI997301 701553168	EST29819	AV678686 AV678686 AZ267308 RPCI-23-4
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BB357781 184 bp mRNA EST 12-JUL-2000 BB357781 RIKEN full-length enriched, adult male corpus striatum Mus musculus cDNA clone C030024G02 3', mRNA sequence. BB357781 GI:9069609 EST. house mouse.
BB357781 184 bp mRNA BB357781 RIKEN full-length enriched, musculus cDNA clone C030024G02 3', ml BB357781 GI:9069609 BEST. house mouse.
BB357781 BB357781 RIK MUSCULUS CDN BB357781 BB357781.1 BR357781.1 BR357781.1
RESULT 1 BB357781/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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                                                             Query Match
Best Local Similarity 63.69
Matches 14; Conservative
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 34
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        Email: genome-resertc.riken.go.jp,
URL:http://genome-resertc.riken.go.jp,
URL:http://genome-rtc.riken.go.jp,
URL:http://genome-rtc.riken.go.jp,
Carillori.P., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayshizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carnlnci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Haysakizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carnlnci,P. and Haysakizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'clone_lib="RIKEN full-length enriched, adult male corpus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                                                                                                                                                                                                                                                                                                                                              The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                             3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="corpus striatum"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C030024G02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
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ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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FEATURES

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/Acce="Vector: palescript II XR; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from inmature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XLIO-Gold host cells, This library was
                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L (bases 1 to 210)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Mattin, J., Beck, C.,
Wylie, T., Underwood, K., Steptoe, M., Theislang, B., Allen, M., Bowers
A.Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                              sn35a01.yl Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1016-13441 5' similar to TR:Q9ZVI3 Q9ZVI3 PUTATIVE ELONGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta; eudicotyledons, core eudicots, Rosidae, eurosids I;
Fabales, Fabaceae, Papilionoideae, Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkway Circle St. Louis, Missouri 63134 For further information earl: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@enomesystems.com or info@enomesystems.com web site: www.genomesystems.com Seq primer: 40RF from Gibco High quality sequence stop: 165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transformed into XL10-Gold host cells, This library was constructed by Dr. Randy Shoemaker and Dr. John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="immature flowers of field grown plants"
/lab_host="XL10-Gold"
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1016-13441"
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                                                                          ö
Length 184;
                                                                          Indels
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   Score 14; DB 128;
Pred. No. 6.5e+02;
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                                                                                                                                   1 tgttggannnnnntttgata 22
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63.68;
63.68;
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TAG\_SEQ=CAAGG"

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ORIGIN

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/GL_xref="Laxon:10090"
/db_xref="Laxon:10090"
/clone="lu" Blat bav-a-11-0-UI"
/dow_stage="lu" Blat bav-a-11-0-UI"
/dow_sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Chin, H
National Institute of Mental Health
(801) Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
The sequence contained an oligo-dr track that was present in the oligoucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site strand cDNA and therefore this may represent he NotI site olfactory bulbs tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESERCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLYA-Ves.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       BE956026 228 bp mRNA EST 04-OCT-2000 UI-M-BH4-bav-a-11-0-UI.SI NIH_BMAP_M_S5 Mus musculus cDNA clone UI-M-BH4-bav-a-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 228)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                          Gaps
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                 DB 134; Length 210;
                                                                                                  8; Indels
            Score 14; DB 134;
Pred. No. 6.7e+02;
0; Mismatches
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TAG_LIB=NIH_BMAP_M_S5
TAG_TISSUE=olfactory-bulbs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
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    63.6%;
63.6%;
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Query Match
Best Local Similarity
Matches 14; Conserv
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom!;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom!;

I (bases 1 to 235)
S (onno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
'P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Natsuyama, T., Maki, K., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya
'Y., Suzuki, H., Suzuki, M., Watanabe, S., Yamamura, T., Yamanaka, I.,
'Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
RIKEN Mouse ESTS (Konno, H., et al.)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fmail: genome-resertc riken.go.jp,
URL:http://genome-resertc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Carninci.P. Nishiyama.Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Yomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                            BB170254 EST 29-JUN-2000 BB170254 RIKEN full-length enriched, adult male hypothalamus Musculus cDNA clone A230017D13 3', mRNA sequence.
                                                                                                                                                                                             Gaps
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/clone="A230017D13"
/clone_lib="RIKEN full-length enriched, adult male
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                                                                                                                           Length 228;
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                           Score 14; DB 138;
Pred. No. 6.8e+02;
0; Mismatches 8;
               75
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Best Local Similarity 63.64
Matches 14; Conservative
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/tissue_type="mammary gland"
/lab_host="DH10B"
/sex="female (lactating)"
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/db_xref="taxon:9606"
/clone_lib="070029"
/dev_stage="Adult"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 250)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                          /lab_host="bloot="15" site_2: BamHI; cDNA library was note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was primed with a primer [5' contributed with a primer [6'] contributed with a primer
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IMAGE:1401067 5' similar to SW:Y335_MYCGE P47577 HYPOTHETICAL
GTP-BINDING PROTEIN MG335.;, mRNA sequence.
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Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.6%; Score 14; DB 102; Length 235; 63.6%; Pred. No. 6.9e+02; Live 0; Mismatches 8; Indels
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/db_xref="taxon:10090"
/clone="IMAGE:1401067"
/clone_llb="Soares_mammary_gland_NMLMG"
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High quality sequence stop: 225.
Location/Qualifiers
1. .250
                         /tissue_type="hypothalamus"
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The WashU-HHMI Mouse EST Project
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Anote—"Vector: pTTT3D-Pac (Pharmacia) with a modified polylinker; 1st strand CDNA was prepared from mammary polylinker; 1st strand CDNA was prepared from mammary pland tissue from a lactating female, and was then primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
Frax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-Qv3-OT0029-290 seq primer: puc 18 forward
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Bukaryota, Matazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 261)
Dias Neto.E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Coldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW879900 261 bp mRNA EST 23-MAY-2000
QV3-OT0029-290300-134-b02 OT0029 Homo sapiens CDNA, mRNA sequence.
AW879900
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shorgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 6.9e+02;
0; Mismatches 8; Indels
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AA515145.1 GI:2254745
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63.68;
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Best Local Similarity 63.69
....hes 14; Conservative
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Unpublished (1997)
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ENKATOGAS, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 265)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, F., Enkuda, T., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Kajosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, M., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, K., Shipata, Y., Shigemoto, Y., Shinagawa, A., Shizaki, T., Sogabe, Y., Sugahara, Y., Sunoda, Y., Wataniki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Yano, K., Yasuishi, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Yano, K., Yasuishi, H., Yaokota, T., Yamanura, T., Yamanuka, I., Yano, H., W., Wokota, T., Yamanuka, T., Yamanuka, T., Yamanuka, T., Killingha, K., Kokota, T., Yamanuka, T., Yananaka, T., Yamanuka, T., Yamanuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fmail: genome-resertc.riken.go.jp,
URL:http://genome-resertc.riken.go.jp,
URL:http://genome-resertc.riken.go.jp,
Carninci.P. vishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
V. v. Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama.J., Shibata,K., Izawa,M., Rawai,J.,
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
Highh-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshinid Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
                                                                                                                                                                                                             Gaps
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                                                                                                                                        DB 96; Length 261; 7e+02;
                                                                                                                                                                                                8; Indels
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                 Score 14; DB 9
Pred. No. 7e+02
0; Mismatches
                  89
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/dev_stage="2 cells"
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63.6%;
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            84
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      79
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Best Local S
Matches 14,
BASE COUNT
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SOURCE
ORGANISM
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COMMENT

FEATURES

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information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( Dases 1 to 298)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute; Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA515145 298 bp mRNA EST 20-AUG-1997 ng68c01.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939336 similar to contains Alu repetitive element; contains element MSR1 repetitive element; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contest: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Probert_Strausbergenih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA cibrary Arrayed by: Greg Lennon, Ph.D.
CDNA cibrary Arrayed by: Greg Lennon, Ph.D.
CLONE distribution: NoT-GGAP clone distribution information www-bio.lnl.gov/Dbrp/image/image.html
Seq priner: -40ml3 fwd. ET from Amersham
High quality sequence stop: 295.
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Pred. No. 7e+02;
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/tissue_type="11posarcoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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56:5380-5383."
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BASE COUNT

ORIGIN

Matches

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other_GSSS: RPCI-23-364L15.TJ
Cother_GSSS: RPCI-23-364L15.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.igr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 364 row: L column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoR1; Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECOR1 sites. The ligation products were transformed into
DHOR electrocompeted tells (BRL Life Technologies).
                                                                                                  A2037213 336 bp DNA GSS 01-MAR-2000
RPCI-23-364L15.TV RPCI-23 Mus musculus genomic clone RPCI-23-364L15
                                                                                                                                                                                                                                                                                                                                                                                           Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 336)
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NSV546877 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
CDNA clone RZLZlal2F 3', mRNA sequence.
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0; Mismatches 8;
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63.6%; Pred. No. 7.4e+02;
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/clone="RPCI-23-364L15"
/clone_lib="RPCI-23"
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/lab_host="DH10B"
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     157 TGTTGGATTGATGGGTTTGATA 178
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AUTHORS
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JOURNAL
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Magnollophyta; eudicotyledons, core eudicots, Rosidae; eurosids I;
Fabales, Fabaceae, Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 332)
VandenBosch, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L.,
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="genotype A17"
/db_xref="texon:3880"
/clone="pkV1-3023"
/clone_lib="kV1"
/tlssuc_type="Seedling roots"
/dev_stage="24 hours post-inoculation with Sinorhizobium mellioti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESTs from roots of Medicago truncatula 24 hours after inoculation with Sinorhizobium meliloti
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EST402778 KV1 Medicago truncatula CDNA clone pKV1-3023, mRNA
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                                                                                                  Length 298
                                                                                               Score 14; DB 8; Length 298
Pred. No. 7.2e+02;
0; Mismatches 8; Indels
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Texas A&M University:T262522e
TIGR sequence name:MTAE96TK
More information is available at.
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. coli strain XLOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: VandeiBosch K
Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
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BE202756
BE202756.1 GI:8746021
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63.68;
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ORGANISM

REFERENCE AUTHORS JOURNAL

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TITLE

FEATURES

ACCESSION VERSION KEYWORDS SOURCE

BE202756

RESULT

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Gaps

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BASE COUNT ORIGIN

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SOURCE

COMMENT

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/lab_host="E. coli BM25.8"

//note="Organ: shoot tips: Vector: Lambda TriplEx; Site_1:
SfiI (A): Site_2: SfiI (B): Shoot tips (approx. 2 cm from
apex) were collected during the spring, frozen and used
for mRNA isolation. The SMARY-PCR method (Clontech) was
used to prepare a library from 1 ug total RNA, using the
Lambda TriplEx vector. Plasmid subclones in pTriplEx were
recovered by cre-lox excision in E. coli strain BM25.8 and
a 48 c 74 g 136 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 371)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Usenter, J.C.

Wenter, J.C.

Map Building
Unpublished (1998)

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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Clones are availabe from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
69 c 85 g 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ311167 371 bp DNA GSS 22-DEC-1998
CITBI-E1-2525E11.TR CITBI-E1 Homo sapiens genomic clone 2525E11,
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Pred. No. 7.5e+02;
0; Mismatches 8; Indels
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ilarity 63.6%; Pred. No. 7.5e+02;
Conservative 0; Mismatches 8;
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/clone="2525E11"
/clone_lib="CITBI-E1"
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A0311167.1 GI:4042980
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Best Local Similarity 63.6
Matches 14; Conservative
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Matches 14; Conserv
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                                                                               Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 359)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Alarge scale analysis of CDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected CDNA libraries

20363093
                                                                                                                                                                                                                                                                                                                                                                              Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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AW226052, GI:6555348
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/db_xref="taxon:3352"
/clone="ST76G08"
/clone_lib="Pine TriplEx shoot tip library"
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Seg primer: 5' lambda TriplEx2 Sequencing Primer.
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/organism="Arabidopsis thallana"
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Pred. No. 7.5e+02;
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/db_xref="taxon:3702"
/clone="RZL21a12F"
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Fax: 919-515-7801
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                                                             thale cress.
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Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Liliopsida; Poales; Poaceae; Zea.
Magnollophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 376)
Rabinowicz,P.D., Schutz,K., Dedhia,N., Yordan,C., Parnell,L.D.,
Stein,L., McComble,W.R. and Martienssen,R.A.
Differential methylation of genes and retrotransposons allows
shotgun sequencing of the maize genome
Nat. Genet. 23, 305-308 (1999)
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 376) Mahahas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                AQ102282 376 bp DNA GSS 27-AUG-1998 HS_3029_A2_G04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=8 Row=M, DNA sequence.
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/db_xref="teaxon:9606"
/clone="plate=3029 Col=8 Row=M"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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an3791J JM101 filtered library Zea mays genomic, DNA sequence.
AQ844476.1 GI:6202964
                                                                                                                                                                                                                                                                                                                                                                                                             scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3039 row: M column: 8
Class: BAC ends
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Contact: Martienssen RA
Cond Spring Harbor Laboratory
1 Bungtown Rd., Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8322
Fax: 516 367 8369
Email: martiens@cshl.org
Seq primer: forward
Class: shotgun.
                                                                                                                                                                                                                                                                                                                        Score 14; DB 163;
Pred. No. 7.5e+02;
0; Mismatches 8;
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Job time: 4588 sec
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Best Local Similarity 63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT:*/cgn2_2/gcgdata/geneseq/geneseqn/NA1995.DAT:*/cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT:*/cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT:*/cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
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/cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                               960044
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                    480022 seqs, 187831343 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                OM nucleic - nucleic search, using sw model
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V58896
T90543
V84598
V59636
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T64683
Q42933
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T39904
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Match Length
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Claim 15; Page 72; 94pp; English.

Score

Result Š. 16.2 16.2 16.2 16.2 16.2 16.2 16.2

264627

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Human OVCA2 tumour Aminopeptidase 012 Aminopeptidase 012

Enterococcus faeca

Human type IV coll

Human secreted pro Breast cancer mamm MMTV env protein n Partial human comp

Human OVCAl tumour

Sh2-mlRev6 gene (s Shrunken-2 gene va Wild-type shrunken

Infection; pathogenic Leptospira; protective immunity; therapy;

L. fainei nucleotide sequence

Leptospira fainei diagnosis; ss.

WO9840099-A1 17-SEP-1998.

20-JAN-1999 (first entry)

V58896;

δŏ q вр

V58896 standard; DNA; 1477

RESULT 758896

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L. fainel. The is bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of LS infections. The DNAs and antibodies may also be used for detection and
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                                                                                               ĽS
       This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species. L. fainei. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and diagnosis of past or present LS infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated pathogenic Leptospira bacterium - useful for, e.g developing products for conferring protective immunity, and for prophylactic or therapeutic treatment
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0
                                                                                                                                                                                                                100.0%; Score 22; DB 19; Length 22; 100.0%; Pred. No. 0.047;
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                                                                                                                                                                 Sequence 22 BP; 7 A; 2 C; 5 G; 8 T; 0 other;
                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                      L. fainei nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-AU00145.
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Best Local Similarity 100.
Matches 22; Conservative
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(AGRI-) AGRIC VICTORIA SERVICES PTY LTD. (PIGR-) PIG RES & DEV CORP.

WPI; 1998-520791/44.

Chappel RJ;

98WO-AU00145 97AU-0005494

06-MAR-1998; 07-MAR-1997;

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                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a Leptospira DNA sequence isolated from the pathogenic Leptospira (LS) bacterium of the invention. The bacterium belongs to serogroup Hurstbridge or serovar hurstbridge or the species L. fainei. The LS bacteria can be used for conferring protective immunity against pathogenic LS bacteria in humans or animals. The bacteria can also be used for prophylactic or therapeutic treatment of infections. The DNAs and antibodies may also be used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                            New isolated pathogenic Leptospira bacterium - useful for, e.g developing products for conferring protective immunity, and for prophylactic or therapeutic treatment
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100.0%; Pred. No. 0.072;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize male fertility gene 233 Zm41-A.
                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 69-70; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 tgttggatcacaagatttgata 22
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Best Local Similarity 100.
Matches 22; Conservative
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T90543/
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100.0%; Score 22; DB 19; Length 22; Larity 100.0%; Pred. No. 0.047; Conservative 0; Mismatches 0; Indels

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06-JUN-1997
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                                                                                                                                                                                                                                                                                                                  This DNA sequence comprises the maize 233 Zm41-A gene. This is an orthologue of Arabidopsis Ms41-A (see 190522), a gene that confers male fertility. It was obtained following a database search for sequences that showed homology to Ms41-A DNA, isolation of a partial cDNA clone, and use of this clone to isolate Zm41-A genes 231 (190542), Z33 (190543) and 235 (190544) from genomic lambda ilbraries. The genes show a high level of conservation. Z35 may be derived from Z31 via genetic rearrangements, deletions and/or insertions. Z33 has subsequent deletions from Z35 and is truncated, having only exons 3, 5 and 6. The Ms41-A and Zm41-A cransgenic plants with controlled male fertility. Male sterile plants with controlled male fertility. Male sterile plants where restoration of fertility is not needed, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                         Nucleic acid encoding proteins involved in male fertility in plants - used to control fertility and for production of hybrid seed
Zm41-A; male fertility; hybrid seed; transgenic plant; antisense;
ribozyme; male sterile; maize; Ms41-A; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2582;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            lettuce, spinach and onions.
                                                                                                                                                                                                                                        Perez P;
                                          Location/Qualifiers
                                                                                                                                                                                                                                        Hodge R,
                                                                                                                                                                                                                                                                                                    Claim 3; Fig 15; 85pp; English.
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1091..1167
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1168..1332
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936..1090
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916..935
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Best Local Similarity 90.0
Matches 18; Conservative
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Human; secreted protein; fusion protein; gene therapy; protein therapy, diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzhelmer's disease; restenosis; AIDS; osteoplate; disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoplast; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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970S-0048970.
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Human secreted protein gene 126 clone HELGH31.

19-JAN-1999 (first entry)

V59636;

V59636 standard; DNA; 1291 BP

RESULT V59636/c

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The invention relates to nucleic acid sequences (V84411 to V84633)

cenceding human secreted proteins (W88534 to W88756). The secreted protein

ce gene sequences are depocated with the ATCC under deposit numbers ATCC

209011, 209080, 209081, 209082, 209008, 209009, 209010, 209011, 209080, 209011, 209080, 209081, 209084, 209085, 209011. Host

cc cells compressing recombinant vectors containing the nucleic acid

sequences are used for the recombinant production of the secreted

crefil for preventing, treating or ameliorating medical conditions e.g.

by determining the amount of the new polypeptides in a sample or by

cc by determining the presence of mutations in the new polynucleotides.

by determining the presence of mutations in the new polynucleotides.

compressing the presence of mutations in the new polynucleotides, based on

which tissues they are most highly expressed in, and include developing

cc specific uses are described for each of the polynucleotides, based on

which tissues they are most highly expressed in, and include developing

createnosis, hepatic and renal diseases, lymphomas, inflammation, allergies,

clischemic shock, Alzateimer's and cognitive disorders, schizophrenia,

createnosis, prostate diseases, obesity, disorders involving osteoclasts

cut has osteoporosis, arthritis or malignancies, diseases of testes, lung

cort thymus, dispersive/endocrine disorders, infections and AIDS. The

colypeptides are also useful for identifying their binding partners.

The present sequence represents a gene encoding a human secreted protein

createnosis, requence represents and clone identification).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 450-451; 772pp; English.
97US-0048901.
97US-0048917.
97US-0048971.
97US-0049019.
97US-004974.
97US-0057627.
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97US-0057774
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P-PSDB; W88721.
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06-JUN-1997;
06-JUN-1997;
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05-SEP-1997;
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05-SEP-1997
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schlarophrenia; prostate; obsety; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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970S-0043578.
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97US-0040626.
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97US-0047492.
97US-0047500.
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97US-0043312.
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97US-0047596.
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97US-0047598.
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                                                                                                                                                    Homo sapiens.
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23-MAY-1997;
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11-APR-1997
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73.6%; Score 16.2; DB 20; Length 951; 85.7%; Pred. No. 47; iive 0; Mismatches 3; Indels 0;

Ouery Match 73.6 Best Local Similarity 85.7 Matches 18; Conservative

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Gaps

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Indels

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Length 1291;

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209048) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Pc portion (e.g. v59501) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: V95311.V5901; amino acid sequences W74731-W75056) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see V55511 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigenic protein; vaccine; Lyme disease; infection; detection; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     B. burgdorferi antigenic protein coding sequence, f893.nt.
                                                                                                                                                                               Sequence 1291 BP; 391 A; 228 C; 203 G; 469 T; 0 other;
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Pred. No. 48;
0; Mismatches
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97US-0050359.
97US-0053344.
97US-0053377.
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Best Local Similarity 85.7%;
Matches 18; Conservative
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20-JUN-1997;
22-JUL-1997;
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P-PSDB; W74854.
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This sequence represents a nucleic acid molecule designated Gene 126 from the human cDNA clone HELGH31 (deposited as clone ATCC 97902 and ATCC

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Best Local Similarity
Matches 18; Conserv
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                                                                            Gaps
                                                                                                                                                                                                                                                                                                                       Maize: acetyl-CoA-carboxylase; fluazifop; sethoxydim; herbicide; probe; transcarboxylase active site: biotin binding site; screening; cassette; antisense; promoter; transit peptide; plasmid; tissue-specific gene expression; herbicide resistance; oilseed; oil content; transgenic plant; crop improvement; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expression cassette containing plant acetyl CoA gene - used to confer herbicide tolerance or to increase oil content of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= Transcarboxylase active site region
59..70
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0
                                             Length 1473;
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 ◆ Sequençe 1473 BP; 622 A; 232 C; 121 G; 498 T; 0 other;
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                                                DB
                                              Score 16.2; DE
pred. No. 49;
0; Mismatches
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                                                                                                                                                                                                                                                                                                     Acetyl-CoA-carboxylase gene fragment
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1770..1946
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88US-0269584.
90US-0538674.
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85.7%;
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                                                   Query Match 73.6
Best Local Similarity 85.7
Matches 18; Conservative
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10-NOV-1988;
18-JUN-1990;
21-JUL-1992;
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Wyse DL;
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promoter, e.g. a cauliflower-mosaic virus 35S promoter or nopaline-synthase promoter, and N-terminal maize chloroplast transit peptide sequence in a plasmid vector for high-level tissue-specific gene expression, to confer herbicide resistance and/or alter the oil content of the plant, or to increase the plant AcCase yield, so that the crystallized enzyme may be used to screen and identify other herbicides that bind to and inhibit the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding maize acetyl coenzyme A carboxylase gene · used for prodn. of plants with herbicide tolerance or altered oil content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acetyl CoA carboxylase; ACCase; herbicide tolerance; cyclohexanedione; aryloxyphenoxypropionic acid; vegetable oil; oilseed; maize; corn; ss.
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                                                                                                                                                                                                                                                                                               Length 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize acetyl CoA carboxylase cDNA clone EcoRI fragment
                                                                                                                                                                                                                   Sequence 2000 BP; 546 A; 406 C; 494 G; 554 T; 0 other;
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Pred. No. 51;
0; Mismatches
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heterologous systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-465030/46.
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays line A188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9631609-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Egli MA,
Wvse DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T39904;
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Gaps

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Indels

Length 2001;

DB 17; 3;

Score 16.2; DE Pred. No. 51; 0; Mismatches

73.6%; |larity 85.7%; |Conservative

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Mycobacterium sp.; internal sequence; intein; immature; gyrase; protein splicing; precursor; gyrA; ss.
                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterial DNA gyrase precursor protein - and polypeptide(s) corresponding to mycobacterial DNA gyrase intein sequences
                                                                                                               M. leprae gyrA precursor coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Pages 33-34; 55pp; French.
                                      T64683 standard; DNA; 3822 BP.
                                                                                                                                                                             Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                       (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-247976/23
                                                                                                                                                                                                                                                                                                                                Cole S, Fsihi H;
                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; W15078
                                                                                                                                                                                                                                                      17-OCT-1995;
                                                                                                                                                                                                                                                                               17-0CT-1995;
                                                                                      17-MAR-1998
                                                                                                                                                                                                     FR2739859-A1
                                                                                                                                                                                                                             18-APR-1997.
                                                             T64683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
              RESULT 11
                           164683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present DNA sequence is a 2kb EcoRI fragment of lamda clone #15-14 including a portion of a maize acetyl CoA carboxylase (ACGSse) gene located at bases 2883 to 83 from the 3' stop codon. AcGase is involved in fatty acid synthesis and is the target of the specified herbicides. Transformation of plants with ACGSse imparts resistance to cyclohexanedione and aryloxyphenorypropanoic acid herbicides and alter the oil content. The ACGASe DNA is also used as source of probes and primers for the identification of transgenic plants; in marker-assisted plant selection and for restriction fragment length polymorphism mapping, used for high-energy animal feed and high-fiber, low-fat human food and in genetic dissection of the groat oil trait.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA encoding acetyl-CoA carboxylase from oats, used to produce transformed plants with herbicide resistance and altered oil content
                                                                                                                                                              EcoRI fragment of lamda clone #15-14 with maize ACCase gene portion.
                                                                                                                                                                                                  maize acetyl CoA carboxylase; ACCase; herbicide; plant oil content; marker-assisted plant selection; groat oil trait; restriction fragment length polymorphism mapping; high-energy animal feed; low-fat human food; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Somers
                                                                                                                                                                                        Herbicide resistance; gene modification; lamda clone #15-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rines HW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 2001 BP; 546 A; 406 C; 494 G; 554 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Groh S, Kianian SF, Phillips RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 10; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   US DEPT OF AGRICULTURE.
EGLI M A.
GROH S.
 22
           249816 standard; DNA; 2001 BP
                                                                                                                                                                                                                                                                                                                                           99WO-US14022.
                                                                                                                                                                                                                                                                                                                                                                   98US-0090240
98US-0091640
2 gttggatcacaagatttgata
                                                                                                                                      18-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        (MINU ) UNIV MINNESOTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIANIAN S F.
PHILLIPS R L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KIAN/) KIANIAN S F.
(PHIL/) PHILLIPS R L.
(RINE/) RINES H W.
(SOME/) SOMERS D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-147205/13.
                                                                                                                                                                                                                                                                                        W09967367-A1.
                                                                                                                                                                                                                                                                                                                                          22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                   22-JUN-1998;
02-JUL-1998;
                                                                                                                                                                                                                                                                                                                    29-DEC-1999
                                                                                                                                                                                                                                                                  Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Egli MA,
                                                                                                                                                                                                                                                                                                                                                                                                                    (USDA )
(EGLI/)
                                                                                                              249816;
                                                             10
                                                                         249816
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95FR-0012162. 95FR-0012162.

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This DNA, isolated from Mycobacterium leprae, encodes a precursor (immature) gyrase protein from which an "intein" (see W15074) is excised during maturation. The gyrase and its coding sequence are useful to fabricate products that alter the maturation of proteins essential for the development of infectious agents by altering the protein splicing of precursor polypeptides of the proteins. The inteins encoded by the gyra genes of Mycobacterium leprae, M. flavescens, M. gordonea and M. kanassii are used: (a) to modify the genome of a eukaryotic cell that lacks endogenous biological activity identical to that of the polypeptide; (b) to replace a copy of a gene present in a recipient genome by integration of a gene different from that where the integration takes place; and (c) for targetted insertion of a foreign by sequence into a selected site in the genome of a eukaryotic cell not containing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3822 BP; 843 A; 899 C; 1092 G; 988 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.2; DE
Pred. No. 54;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        specific cleavage sites of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2334 gttggatcagatgatttgtta 2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 gttggatcacaagatttgata 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q42933 standard; DNA; 4346 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.6%;
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A3 maize ACCase cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         042933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       042933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DXAXAX
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Gaps . 0;

. 0

Indels

3;

Query Match 73.6%; Score 16.2; DB 21; Best Local Similarity 85.7%; Pred. No. 51; Agtches ,18; Conservative 0; Mismatches 3;

2 gttggatcacaagatttgata 22

ö 8

Length 2001;

cyclohexanedione; aryloxyphenoxypropionic acid; vegetable oil;

oilseed; maize; corn; ss.

Zea mays line A188.

Key

Location/Qualifiers 37..7014 /\*tag= a /\*tag= a /EC\_number= 6.4.1.2

Acetyl CoA carboxylase; ACCase; herbicide tolerance;

Maize acetyl CoA carboxylase cDNA

23-JAN-1997

T39905;

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902 gttggatgacaagagttgtta 922

T39905 standard; cDNA; 7470 BP

RESULT 13

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une sequence is used to line As accept con carboxylase (Accase) CUNA maize clone which can be used to probe plant DNA to isolate other such clones. It may be used with plant regulatory sequences to produce expression cassettes for Accase. These cassettes are used to renaposition of seeds or Accase. These cassettes are used to transform plants to downregulate produc of Accase. This can alter the composition of seeds or other plant parts, e.g. enabling oilbearing plants such as oilseed rape, sunflower or oilpalm, having a lower or modified oil content to be produced. It can be used to form expression cassettes for overexpression of Accase, leading to produce of plants with an increased oil content. It may also be used to form expression cassettes for overexpression of Accase, leading to produce of plants with an increased oil content. It may also be used to recover the Accase expression. Monocotyledonous plants can be made tissue-specific or developmentally regulated manner, and this RNA used to inhibit Accase expression. Monocotyledonous plants can be made tesistant to grass weed herbicides adopted to express Accase. This is acheived by overexpression of monocot Accase, expression of dicot Accase (which is relatively tolerant to these herbicides used to provides crop plants which are resistant to herbicides used to provides crop plants which are resistant to herbicides used to applic where there has been short term carryover of herbicide from the provides crop. Using the method, weeds such as wild oats may be controlled, and the farmer is given extra options to obtain an improved harvest using means which are safer, chaaper or more effective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of the A3 acetyl coA carboxylase (ACCase) cDNA
        Acetyl coA carboxylase; ACCase; probe; expression; oil content; lower; modified; increased; oilseed rape; sunflower; resistant; resistance; grass-weed herbicides; fluazifop; alkylketones; maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA clones for use in probing plant DNA - comprise maize acetyl coenzyme-A carboxylase gene flanked by heterologous DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4346 BP; 1239 A; 829 C; 1064 G; 1213 T; 1 other;
                                                                                                                                                                                                                                                                 /*tag= b
/note= "GAN encodes Glu or Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ICIL ) ICI AUSTRALIA OPERATIONS PTY LTD. (ICIL ) IMPERIAL CHEM IND PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whitfeld PR;
                                                                                                                                                            Location/Qualifiers
3..3947
/*tag= a
                                                                                                                                                                                            /*tag= a
/note= "ACCase"
1875.1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 3; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          92WO-GB02205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   91GB-0025330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashton AR, Jenkins CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-197061/24.
                                                                               wheat; barley; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; R36781
                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-1992;
                                                                                                                                                                                                                                                                                                                           WO9311243-A.
                                                                                                                                                                                                                                                                                                                                                                    10-JUN-1993
                                                                                                                        Zea mays.
                                                                                                                                                                Key
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DNA encoding maize acetyl coenzyme A carboxylase gene – used for prodn. of plants with herbicide tolerance or altered oil content

Claim 2; Page 78-80; 131pp; English.

Somers DA;

Gronwald JW, Lutz SM,

Gengenbach BG,

Egli MA, Wyse DL;

WPI; 1996-465030/46.

P-PSDB; W05590

(MINU ) UNIV MINNESOTA

96WO-US04625. 95US-0417089.

04-APR-1996; 05-APR-1995;

WO9631609-A2

10-OCT-1996

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Gaps
                                                                                                                                                                                                                                                                                                                                                                     A cDNA sequence (T39905) codes for maize acetyl CoA carboxylase (ACCase) (W05590), an enzyme that plays a central role in fatty acid biosynthesis and accumulation in plants and seeds. The complete sequence was deduced from cDNA cloue #18-5, obtd. from a lambda gtll cDNA library of maize inbred A188 seedlings, and from PCR amplifications (see also T39918-23). Genomic ACCase DNA fragments have also been isolated (see also T39906-16). ACCase DNA herbicide tolerance or oil content of a transgenic plant, or used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7470 BP; 2119 A; 1429 C; 1844 G; 2071 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.2; DB
Pred. No. 58;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to produce ACCase in heterologous systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3972 gttggatgacaagagttgtta 3992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V29317 standard; cDNA; 7470 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.68;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 gttggatcacaagatttgata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V29317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 v29317
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Gaps

73.6%; Score 16.2; DB 14; Length 4346; 85.7%; Pred. No. 55; Live 0; Mismatches 3; Indels 0;

Query Match
Best Local Similarity 85.7
Matches 18; Conservative

2 gttggatcacaagatttgata 22

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(first entry)

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New DNA encoding acetyl-CoA carboxylase from oats, used to produce transformed plants with herbicide resistance and altered oil content
                                                                                                                      maize acetyl CoA carboxylase; AcCase; herbicide; plant oil content; marker-assisted plant selection; groat oil trait; restriction fragment length polymorphism mapping; high-energy animal feed; low-fat human food; ss.
                                                                                                       Herbicide resistance; gene modification;
                                                                     Maize acetyl CoA carboxylase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Egli MA, Groh S, Kianian SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MINU ) UNIV MINNESOTA.
(USDA ) US DEPT OF AGRICULTURE.
(EGLI/) EGLI M A
(GROH/) GROH S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIANIAN S F.
PHILLIPS R L.
RINES H W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-147205/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOMERS D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; Y44687
                                 18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                               W09967367-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oil trait
                                                                                                                                                                                                                 mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KIAN/)
(PHIL/)
(RINE/)
(SOME/)
249820;
                                                                                                                                                                                                                                                                                                                        5'UTR
                                                                                                                                                                                                                                                                                                                                                            3'UTR
                                                                                                                                                                                                                 zea
                                                                                                                                                                                                                                                 Key
CDS
This cDNA encodes a maize ACCase enzyme. This can be used in a method of preparing an herbicide resistant corn plant to a second corn plant comprises at least 1 herbicide resistant.

C. where the first corn plant comprises at least 1 herbicide resistant allele and the second plant comprises at least 1 herbicide resistant to allele which is not allelic to the herbicide resistant allele present in the first plant. The herbicide resistant corn plants are prepared using Accl and Acc2 gene combinations which impart cylcohexanedione (CHD) or aryloxyphenoxypropanoic acid (APA) herbicide tolerance to the corn plant. The methods are used to impart CHD and APA herbicide tolerance to corn plant. The methods are used to impart CHD and herbicide tolerance to corn plant. The methods are also be used to impart tolerance to a corn plant also be used to impart tolerance to a corn plant to an agent which inhibits acetyl CACA and corn plant to an agent which inhibits acetyloxylase, selected from to all to prophenyl) perhydroindolizine-2,4 dione, 3-isopropyl-6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                  ACCase; maize; herbicide resistant; corn plant; tolerance; Accl; Acc2; cylcohexanedione; CHD; aryloxyphenoxypropanoic acid; APA; enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herbicide resistant corn plants · prepared using Accl and Acc2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -acetamido-1,3,5-triazine-2,4 (1H,3H)dlone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.6%; Score 16.2; DB 19; Length 7470;
85.7%; Pred. No. 58;
1.ve 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parker WB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7470 BP; 2119 A; 1429 C; 1844 G; 2071 T; 7 other;
                                                                                                                                                                                                                                  aa:
aa:
                                                                                                                                                                                                            /*tag= a
/transl_except= (pos:4339..4341,
/transl_except= (pos:4456..4458,
/transl_except= (pos:4359..4461,
/product= "ACCase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marshall LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           soraphen A and their structural analogues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Fig 3A-E; 112pp; English.
                                                                                                                                                                          Location/Qualifiers 37..7014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lutz SM,
                                                  Maize ACCase enzyme encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wyse DL;
                                                                                                                                                                                                                                                                                                                                                                                            97WO-US15344.
                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0697826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.6
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gengenbach BG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [N-[2,2-dimethylpropyl]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vandèe KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MINU ) UNIV MINNESOTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-207043/18.
P-PSDB; W56736.
                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-1996;
                                                                                                                                                                                                                                                                                                                     409808963-A1
                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                combinations
              30-JUL-1998
                                                                                                                                                                                                                                                                                                                                                        05-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Somers DA,
                                                                                                                                          Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Egli MA,
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98US-0090240. 99WO-US14022

/\*tag= a /product= "Maize acetyl CoA carboxylase"

/\*tag= b 7014..7470 /\*tag= c

Location/Qualifiers 37..7014

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                                                        The present cDNA sequence encodes maize acetyl CoA carboxylase (ACCase). ACCase is involved in fatty acid synthesis and is the target of the specified herbicides. Transformation of plants with ACCase imparts resistance to cyclohexanedione and aryloxyphenoxypropanoic acid herbicides and alter the oil content. The ACCase DNA is also used as source of probes and primers for the identification of transgenic plants; in marker-assisted plant selection and for restriction fragment length polymorphism mapping, used for high-energy animal feed and high-fiber, low-fat human food and in genetic dissection of the groat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7470;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7470 BP; 2119 A; 1430 C; 1843 G; 2071 T; 7 other;
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85.7%; Pred. No. 58;
tive 0; Mismatches 3;
Example 6; Fig 13; 197pp; English.
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Best Local Similarity
Matches 18; Conserva
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3972 gttggatgacaagagttgtta 3992

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249820 standard; cDNA; 7470 BP.

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RESULT 15 249820

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Rines HW,

Phillips RL,

Search completed: March 27, 2001, 08:23:02 Job time: 5304 sec

Sequence Sequence Sequence

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ALIGNMENTS

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Sequence 1, Application US/08014326
; Sequence 1, Application US/08014326
; Patent No. 5498544
; GENERAL INFORMATION:
    APPLICANT: Gengenbach, Burle G.
    APPLICANT: Gengenbach, Burle G.
    APPLICANT: Genwald, John W.
    APPLICANT: Egli, Margaret A.
    APPLICANT: Egli, Margaret A.
    APPLICANT: Lutz, Shiela M.
    TITLE OF INVENTION: Method and An Acetyl CoA Carboxylase
    TITLE OF INVENTION: Alteration in Oil Content of Plants
    NUMBER OF SEQUENCES: 4
    CORRESPONDERGE ADDRESS:
    ADDRESSEE: Merchant & Gould
    STREET: 3100 No. 5498544west Center
    CITY Minneapolis
    CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,326
FILING DATE: 05-FEB-1993
CLASSIFICATION NUMBER: US 07/917,462
FILING APPLICATION NUMBER: US 07/917,462
FILING APPLICATION NUMBER: US 07/917,462
FILING APPLICATION NUMBER: US 07/538,674
FILING APPLICATION NUMBER: US 07/538,674
FILING APPLICATION NUMBER: US 07/269,584
FILING APPLICATION NUMBER: US 07/269,584
FILING APPLICATION NUMBER: 36,848
ATTORNEY/AGENT INFORMATION:
NAME: KOWAICHYK KATHETINE M.
REFERRNCE/DOCKET NUMBER: 36,848
REFERRNCE/OCKET NUMBER: 36,848
REFERRNCE/OCKET NUMBER: 36,848
TELEFPAX: 612-332-5300
                                    US-08-204-6568-1
US-08-204-6568-3
US-08-204-6568-5
US-08-470-702-1
US-08-470-702-2
US-08-470-702-4
US-08-467-831-1
US-08-467-831-3
US-08-467-831-3
US-08-467-831-4
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LENGTH: 2000 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                        COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z
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Patent No. 5256642
Patent No. 5472939
Patent No. 5256642
Patent No. 5472939
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26.799 Million cell updates/sec
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Sequence 5, Al
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Sequence 14,
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                                                                                                                                       March 27, 2001, 08:19:23; Search time 132.3 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-485-241-1
US-08-874-162-1
US-08-399-986B-3
US-08-399-986B-1
US-08-399-986B-1
US-08-493-754A-1
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US-08-119-361-4
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Listing first 45 summaries
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22
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Maximum DB seq length: 200000000
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Match Length
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FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN
OIL CONTENT OF PLANTS
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                                                                                                                                  DB 1; Length 2000;
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APPLICANT: Wyse, D. L.
APPLICANT: Growald, J. W.
APPLICANT: Egli, M. A.
APPLICANT: Litz, S. M.
APPLICANT: Litz, S. M.
APPLICANT: Litz, S. M.
TITLE OF INVENTION: METHOD FOR PRODUCING PLANT ACETYL COANUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A. STREET: P.O. Box 2938
CITY: Minneapolis
STATE: W. COUNTRY: USA
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                                                                                                                                                                         Indels
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OPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: 2 kb fragment of lambda clone #15-14
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                                                                                                                                73.6%; Score 16.2; I
85.7%; Pred. No. 20;
tive 0; Mismatches
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Pred. No. 20;
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Patent No. 6146867
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Patent No. 6069298
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2001 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.6' Best Local Similarity 85.7' Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
TITLE OF INVENTION: FOR
TITLE OF INVENTION: OIL
NUMBER OF SEQUENCES: 11
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy di
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                                                                                                                                                                           Conservative
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Matches 18; Conserva
  linear
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TOPOLOGY:
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                                                                          US-08-014-326-1
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                                                                                                                                    Query Match
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APPLICANT: JENKINS, COLIN L.D.
APPLICANT: WHITFELD, PAUL R.
TITLE OF INVENTION: MAIZE ACETYL COA CARBOXYLASE ENCODING
TITLE OF INVENTION: DNA CLONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOAPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                           APPLICATION NUMBER: US/08/695,651
FILING DATE: 12-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/244,537
FILING DATE: 18-AUG-1994
CLASSIFICATION: 800
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                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/417089
FILING DATE: 05-APR-1995
                                                                                                                                                                                            APPLICATION NUMBER: 08/014326
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 07/917462
FILING DATE: 21-JUL-1992
APPLICATION NUMBER: 07/538674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-244-537-1; Sequence 1, Application US/08244537; Patent No. 5854420; GENERAL INFORMATION:
                      SYSTEM: DOS
FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                    NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 601
                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
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85.7%;
COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                             FILING DATE: 18-JUN-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001 base pairs
                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     612-339-3061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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Best Local Similarity
Matches 18; Conserv
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No. of Street, or other Persons and Person

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Score 16.2;
Pred. No. 23;
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,651
FILING DATE: 12-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/417089
FILING DATE: 05-APR-1995
APPLICATION NUMBER: 08/014326
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 07/917462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 600.318US3
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; Sequence 14, Application US/08602145
; Patent'No. 6025336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/917462
FTLING DATE: 21-JUL-1992
APPLICATION NUMBER: 07/538674
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3972 GTTGGATGACAAGAGTTGTTA 3992
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TELEPHONE: 612-373-6900
                                                                                                                                                                                                                                                                   ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,
                            myse, D. L.
Gronwald, J. W.
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Best Local Similarity 85.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: single
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                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                           Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
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US-08-695-651-5
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STREET: 30
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FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN
OIL CONTENT OF PLANTS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,089
INFORMATION FOR SEQ ID NO: 5:
            PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB92/02205

ATTORNET AGENT INFORMATION:
NAME: VAGENT INFORMATION:
NAME: KOKULIS, PAUL N.
FREISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 203094/SEE 36663/UST
TELEPHONE: (202) 861-3000
TELEPHONE: (202) 861-3000
TELEPHONE: (202) 861-3000
TELEPHONE: (202) 861-3000
TELEPHONE: 4714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4345 base pairs
TYPE: nucleic acid
STRANDENNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.2;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.6%; Score 16.2;
85.7%; Pred. No. 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-695-651-5
; Sequence 5, Application US/08695651
; Patent No. 6146867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08417089 Patent No. 6069298
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US-08-417-089-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 73.6%;
Best Local Similarity 85.7%;
Matches 18; Conservative
28-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 7470 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: Gengenbach, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 73.6
Best Local Similarity 85.7
Matches 18; Conservative
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TITLE OF INVENTION: METH
TITLE OF INVENTION: OIL
TITLE OF INVENTION: OIL
UNDBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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APPLICANT: Greenberger, Joel S.
TITLE OF INVENTION: DETERMINING EXPOSURE TO IONIZING RADIATION
TITLE OF INVENTION: AGENT WITH PERSISTENT BIOLOGICAL MARKERS
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TITLE OF INVENTION: METHOD FOR PRODUCING PLANT ACETYL COA
                                                                                                   E: Schwegman, Lundberg, Woessner & Kluth, P.A. P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Gaps

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APPLICANT: Elliott, Luanne
APPLICANT: Elliott, Luanne
APPLICANT: Elliott, Luanne
APPLICANT: Ksiazek, Thomas G.
APPLICANT: Nichol, Stuart T.
APPLICANT: Morzunov, Sergey
APPLICANT: Morzunov, Sergey
APPLICANT: Ravkov, Eugeny
TITLE OF INVENTION: The Black Creek Canal Hantavirus and
TITLE OF INVENTION: Related Methods
NUMBER OF SEQUENCES:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 127 Peachtree Street, N.E., Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.6; DB 1; Length 1096;
Pred. No. 37;
0; Mismatches 4; Indels 0
                                                                                                                                                                                               LOCATION: 144 to 841
CTHER INFORMATION: the coding region shown in (2)(ix)(B)
CTHER INFORMATION: codes for the protein of SEQ ID NO: 3
US-08-684-862-8
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
CLASSIFICATION NUMBER:
PRICK APPLICATION NUMBER:
TELING DATE:
NAME:
APPLICATION NUMBER:
APPLICATION NUMBER:
TELEBROCKET NUMBER:
TELEBROCKET NUMBER:
TELEBROCHER (404) 688-0770
                                                                                                              MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Agkistrodon rhodostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08792055
Patent No. 5853980
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IBM PC compatible
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1989 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 70.9%;
Best Local Similarity 81.8%;
Matches 18; Conservative
LENGTH: 1096 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                 nucleic acid
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                                                                                            TOPOLOGY: linear
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                                                             STRANDEDNESS:
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FITTLE OF INVENTION:
FITTLE OF INVENTION:
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                                 COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: 18M AT-compatible, 80286 processor OPERATING SYSTEM: MS-DOS version 5.0 SOFTWARE: WordPerfect version 5.1 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/684,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
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Pred. No. 31;
0; Mismatches
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PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,040
FILING DATE: 30-DEC-1992
APPLICATION NUMBER: PCT/EP91/01361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-684-862-8/c
; Sequence 8, Application US/08684862
; Patent No. 5759541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 81.8%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELERA: (202)672-5349
TELEX: 904136
INFORMATION FOR EGD ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 296 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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                  20007-5109
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D.C.
USA
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STRANDEDNESS:
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CORRESPONDENCE ADDRESS:
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                                    70.9%; Score 15.6; DB 2; Length 1989; 81.8%; Pred. No. 39;
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                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hannah, L. Curtis
APPLICANT: Hannah, L. Curtis
APPLICANT: Giroux, Michael
TITLE OF INVENTION: Materials and Methods for Increasing
TITLE OF INVENTION: Corn Seed Weight
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Materials and Methods for Increasing Corn Seed Weight
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                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Saliwanchik & Saliwanchik STRRET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STRTE: FL COUNTRY: USA ZIP: 32606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Patent No. 5650557
GENERAL INFORMATION: APPLICANT: Hannah, L. Curtis
APPLICANT: Giroux, Michael
                                                                                                                                                                                                                                                             Sequence 1, Application US/08299675 Patent No. 5589618
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                                                                                                                                          288 TGTTGGATCAACAGATTTTGTA 267
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                                                                                                                    1 tgttggatcacaagatttgata 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-299-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7745 base pairs
                                                         Best_Local Similarity 81.8
Matches 18; Conservative
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Matches 18; Conservative
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TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-485-241-1/c
                                                                                                                                                                                                                        RESULT 10
US-08-299-675-1/c
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                                      Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08874162
Patent No. 5872216
GENERAL INFORMATION:
APPLICANT: Hannah, L. Curtis
APPLICANT: GIROUX, Michael
TITLE OF INVENTION: Corn Seed Weight
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2: Saliwanchik, Lloyd & Saliwanchik
2421 N.W. 41st Street, Suite A-1
:: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 46;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.9%; Score 15.6;
81.8%; Pred. No. 46
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION. ....
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,675
FILING DATE: 1-SEP-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/874,162
FILING DATE: 13-JUN-1997
                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3600 TGTTGGATAACAAGATGACATA 3579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: DNA (genomic) US-08-485-241-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 7745 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
               STREET: 2421 n...
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Gainesville
STATE: FL
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                                                          STATE: FL
COUNTRY: US
ZIP: 32606
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Gaps

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Godwin, Andrew K.
VENTION: No. 5801041el Gene Associated with Suppression
VENTION: of Tumor Development
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Godwin, Andrew K.
TITLE OF INVENTION: No. 5821338el Gene Associated with Suppression
TITLE OF INVENTION: of Tumor Development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1016;
                                                    Score 15.2; DB 1; Length 1016; Pred. No. 57; 3; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.2; DE
Pred. No. 57;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/493,754A FILING DATE: 22-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              Sequence 3, Application US/08493754A Patent No. 5821338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-399-986B-1/c
; Sequence 1, Application US/08399986B
; Patent No. 5801041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1016 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         830 TTGGGTCTCAAGAATTGATA 811
                                                                                                                                                                830 TTGGGTCTCAAGAATTGATA 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 3:
                                                         69.1%;
85.0%;
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85.0%;
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Best Local Similarity 85.0
Matches 17; Conservative
                                              Ouery Match
Best Local Similarity 85.07
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: GODWIN
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Godwin
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US-08-493-754A-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE:
US-08-493-754A-3
US-08-399-986B-3
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APPLICANT: Godwin, Andrew K.
TITLE OF INVENTION: No. 5801041el Gene Associated with Suppression
TITLE OF INVENTION: Of Tumor Development
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 7745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: PARTON COUNTY: USA
COUNTY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,986B
FILING DATE: O6-MAR-1995
CLASSIFICATION: 530
ATTOREX/AGENT INFORMATION:
NAME: Hagan, Patrick J, 63
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-404
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.9%; Score 15.6; I 81.8%; Pred. No. 46; tive 0; Mismatches
                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,675
FILING DATE: 1-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R. R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: UF-146C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFPHONE: 352-375-8100
  US 08/485,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08399986B
Patent No. 5801041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3600 TGTTGGATAACAAGATGACATA 3579
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                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-874-162-1
                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1016 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
                7-JUN-1995
                                                                                                                                                                                                                                                                                                                          7745 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
    APPLICATION NUMBER:
                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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US-08-399-986B-3/c
                                                                                                                                                                                                                                                                                                                          LENGTH:
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Gaps

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street
CITY: Philadelphia
STREET: 1601 Market Street
CITY: Philadelphia
STREET: 1601 Market Street
COUNTRY: Philadelphia
TYPE: 19103-2307
COMPUTER READALE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: THE FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENALE #10, Version #1.30
SOFTWARE: PARENALE PORMSE: 105/08/399,986B
FILING DATE: 06-MAR-1995
CLASSIFICATION NUMBER: 27,643
FELECHANICATION NUMBER: 27,643
FELECHANUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEPHONE CARACTERISTICS:
LENGTH: 2182 base pairs
TYPE: nucleic acid
STRANDEDRESS: double
TYPE: DNA (genomic)
HYPETICAL: NO
ANTI-SENSE: NO
US-08-399-966B-1
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 Query Match
 69.1%;
 Score 15.2;
 DB 1;
 Length 2182;

 Best Local Similarity
 85.0%;
 Pred. No. 62;
 3 Indels
 0;

 Matches 17;
 Conservative 0;
 0;
 Mismatches 3;
 1ndels 0;

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Search completed: March 27, 2001, 08:19:25 Job time: 5152 sec

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em_esthum11:*
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em_estp11:
em_estp12:
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gb_est44:
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100:
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                                                                 March 27, 2001, 07:38:25; Search time 2517.78 Seconds (without alignments) 61.230 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                             7991742 seqs, 3503743858 residues
                                                                                                                                                 1 tgttggatcacaagatttgata 22
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Maximum Match 100%
Listing first 45 summaries
                                                 OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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gb_est38:*
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em_estba:*
em_estba:*
em_estfun:*
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9b_est2:**
9b_est5:**
9b_est6:**
9b_est6:**
9b_est6:**
9b_est10:**
9b_est20:**
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                                                                                                                       Title:
Perfect score:
Sequence:
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                                                                         Run on:
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Description

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AV532040 .226559 AB038725 AV520789 AI995637 BE977618

SUMMARIES

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AV532040 361 bp mRNA EST 01-SEP-2000 AV532040 Arabidopsis thaliana flower buds Columbia Arabidopsis thaliana cDNA clone FB034f09F 3', mRNA sequence. AV532040 AV532040.1 GI:8692323 EST. thale cress.
                                                                                                                                                  pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                        gb_gss26:*
gb_gss27:*
gb_gss28:*
gb_gss25:*
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Query
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190:
191:
192:
193:
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em_estrol8:*

gb_est58:*

gb_est59:*

gb_est60:*

gb_est61:*

gb_est61:*

gb_est65:*

gb_est65:*

gb_est65:*

gb_est65:*

gb_est66:*

gb_est76:*

gb_est78:*

gb_est81:*

gb_est81:*
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em_estro15:*
em_estro16:*
                 em_estpl6:*
em_estpl7:*
em_estpl8:*
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em_gss6:
em_gss7:
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AV532040 AV532040
226559 ATTS1651 Ve
AB038725 AB038725
AN520789 AV620789
A1995637 701676626
BE977018 B656108.Y
AL190387 Tetracodon
BF006254 EST434942
BF28044 EST434942
BF28120 K451207.Y
AQ497719 HS\_506\_B
BE281304 601101323
BE283045 601101323
BE283045 601101323
BE2823045 601101323
BE642809 Cr12\_7\_B0
AL077427 Drosophil
BE068225 MF48 EF036
AL077427 Drosophil
AQ55814 HS\_213\_B
AQ55814 HS\_213\_B
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AQ55814 HS\_2010\_A
AQ55814 HS\_2010\_A
AQ55814 HS\_2010\_B
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BF177514 EST260593
BG7515 T22M10TR TA
AT77705 EST35611
AW631332 A931332
BG7515 T22M10TR
AU77705 EST35600
BE18999 UI-R-CAO-T20862 GC01908-C7
AW649764 500004C01
AU761541 Wf616107.X
BF002933 7951009-X

ALIGNMENTS

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Gaps

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Length 394;

us-09-380-826a-7.rst

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Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 490)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Columbia"
/db_xref="taxon:3702"
/clone="Apr309031_f"
/clone=lib="Arabidopsis thaliana Above-ground organ from two to six-week old plants Columbia"
/fissue_type="Above-ground organ from two to six-week old plants"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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                                                                                                                                                                                                                                                                        AB038725 490 bp mRNA EST 29-SEP-2000 AB038725 Arabidopsis thaliana Above-ground organ from two to six-week old plants Columbia Arabidopsis thaliana cDNA clone APZ30903_f 3', mRNA sequence.
                                                              DB 147;
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    490
    /organism="Arabidopsis thaliana"

                                                          Score 18.8; DE
Pred. No. 35;
0; Mismatches
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||||||| ||||||||||| |
321 TGTTGGTTCACAAGATTTGACA 300
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                                                                                                                                                                                                                                                                                                                                                                         AB038725.1 GI:7212552
                                                            85.5%;
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Arabidopsis thaliana
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Arabidopsis thaliana
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                                                          Query Match 85.5
Best Local Similarity 90.9
Matches 20; Conservative
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MEDLINE
COMMENT
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TITLE
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      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 361)
Asamizu, E., Nakamura; Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana; Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="versailles-vc"
/tissue_lype="whole seedlings"
/dev_stage="in vitro-grown etiolated seedlings,5 days old"
/note="vertor: pBluescript" 133 t 1 others
                                                                                                                                                                                                                       The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; endicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Arabidopsis thaliana flower buds Columbia"
/tissue_type="flower buds"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226559 394 bp mRNA EST 31-MAY-1995 ATTS1651 Versailles-VC Arabidopsis thaliana cDNA clone VCVDH08 3' similar to Ribonuclease (RNS2), mRNA sequence. 226559 226559.1 GI:404227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Arabidopsis thaliana transcribed genome: the GDR cDNA program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
Contact: Desprez T., Amselem J., Chiapello H., Rouze P., Caboche
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0
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Pred. No. 34;
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Route de Saint-Cyr, 78026 Versailles
Email: thierry@versailles.inra.fr.
Location/Qualifiers
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0; Mismatches
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/db_xref="taxon:3702"
/clone="VCVDH08"
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/clone="FB034f09F"
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                                                                                                                                                                                                                                                                                                                                                                       /strain="Columbia"
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AUTHORS TITLE

REFERENCE

JOURNAL MEDLINE

COMMENT

FEATURES

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Drosophila motive.
Unpublished (1999)
Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg, 6, Rm Bl-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: oliver@hellx.nih.gov,
http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabates and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Commanding Center (NISC; see http://www.nisc.nih.gov).
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//lab_host="SOLR (Stratagene)"
/note="Organ: testis; Vector: pBlueScript SK (Stratagene);
Site_1: ECOR I; Site_2: Xho I; Testes dissected from 1-5
day adult y[*] w[67c1]/Y males raised at 25oC. RNA
isolated using Trizol (Life Technologies) and a single
                                                                                                                                    /note="Vector: psport; Site_1: Not!; Site_2: Sall; cDNA library was derived from untreated inflorescence tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 peach constant light, and watered with fertilizer. CDNA synthesis was initiated using a NotI-oligo(dT) primer. Synthesis was initiated using a NotI-oligo(dT) primer, digested with NotI, size-selected, and cloned into the NotI and Sall sites of the pSPORT vector."
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/sex="male"
                    /clone="701676626"
/clone_lib="A. thaliana, Columbia Col-0, inflorescence-1"
/tissue_type="inflorescence"
/dev_stage="4 - 7 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 608) Andrews, J., Bouffard, G. and Oliver, B. Drosophila melanogaster testis expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.5%; Score 18.8; DB 27; 90.9%; Pred. No. 36;
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Seq primer: M13RP1 reverse primer (ABI).
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/db_xref="taxon:7227"
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 527)
Asamlzu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of CDNA in, Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
                                                                                                                                                                                                                                                                                                         The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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701676626 A. thallana, Columbia Col-0, inflorescence-1 Arabidopsis
thallana CDNA clone 701676626, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Arabidopsis thaliana aboveground organs two
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Tel: 877-577-2733
Fax: 314-427-3324
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/cultivar="Columbia Col-0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3702"
/clone="AP232g06F"
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90.9%;
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BASE COUNT ORIGIN

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REFERENCE AUTHORS TITLE JOURNAL

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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSO2BWA 934 bp DNA GSS 12-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
254C22 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Burypterygii; Chenosquamata; Acanthomorpha; Buacanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon. 1 (bases 1 to 934)

1 (bases 1 to 934)

Soost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J.
round of Poly(A)+ selection using Oligotex (Qiagen). CDN
library constructed using Stratagene ZAP-CDNA syntesis
kit. Oligo df-primed, size fractionated -1-6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
Following a single round of amplification pBlueScript SK
phagemids were mass excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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/note="Genoscope sequence ID : C0AG254BB11SP1-end
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Pred. No. 62;
                                                                                                                                                                                                                                                                Length 608;
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/db_xref="taxon:99883"
                                                                                                                                                                                                                                                              83.6%; Score 18.4; DB 138;
95.0%; Pred. No. 59;
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                                                                                                                                                                                                                                                                                                      0; Mismatches
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GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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95.0%;
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/tissue_type="leaves and cotyledons"
/descatege="mixture of cotyledons from five days old
plants and leaves obtained from two weeks old plants.
/lab_host="E. coll strain SOLR"
/lab_host="E. coll strain SOLR"
/note="Vector: pBluescript SK +/-: Site_1: EcoRI: Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from the
mixture of cotyledons of five days old plants and leaves
of two weeks old plants. The cDNA was directionally
ligated into the Uni-ZAP XR vector from Stratagene and
packaged using Glapack III Gold packaging extracts.
Plasmids containing cDNA inserts were excised from the
recombinant lambda-ZAP phage using Ex-Assist helper phage
and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Paplilonoideae; Medicago.
                                                                                                                                                                                   BF006444 600 bp mRNA EST 06-OCT-2000 EST434942 DSLC Medicago truncatula CDNA clone pDSLC-41J15, mRNA
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University of Minnesota name: M275482e TIGR sequence name:
WTLBA56TK Wore information is available at:
http://chrysie.camu.edu/medicago
Seq primer: Skmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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Fedorova, M., Pierson, B.L., Samac, D.A., Gantt, J.S., v Gonzales, M.B. and Ellis, L.
ESTS from Medicago truncatula leaves and cotyledons Unpublished (2000)
Contact: Deborah A. Samac
University of Minnesota
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Pred. No. 1.2e+02;
0; Mismatches 2; 1
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BF006444.1 GI:10706719
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BF006254/c
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Email: genome-resettc.riken.go.jp,
URL:http://genome-resettc.riken.go.jp,
URL:http://genome-rtc.riken.go.jp,
Caninoi.P. Nishlyama.Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki
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Please visit our web site (http://genome.rtc.riken.go.jp) for
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojia, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Tozuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Y., Yano, R., Yasunishi, A., Yokota, T., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Upublished (2000).

Inpublished (2000).

Contact: Yoshihide Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
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/dev_stage="mixture of cotyledons from five days old
plants and leaves obtained from two weeks old plants"
/lab host="E. col! strain SOLR"
/note="vector: pBluescript SK +/-; Site_1: EcoRI; Site_2:
xhoi; cDNA was prepared from polyA+ enriched RNA from the
mixture of cotyledons of five days old plants and leaves
of two weeks old plants. The cDNA was directionally
ligated into the Uni-ZAP XR vector from Stratagene and
packaged using Gigapack III Gold packaging extracts.
Plasmids containing cDNA inserts were excised from the
recombinant lambda-ZAP phage using Ex-Assist helper phage
and propagated in SOLR cells."

48 a 132 c 124 g 229 t.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
101 Serlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
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BB288727 RIKEN full-length enriched, 2 cells egg Mus musculus CDNA
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Końno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
                                                                                                                                                                                                                            core eudicots; Rosidae; eurosids I;
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University of Minnesota name: M275292e TIGR sequence name:
MTLAN47K More information is available at:
http://chrysie.tamu.edu/medicago
Seq primer: Skmod (CTP gAA CTA gtg gAT CC).
Location/Qualifiers
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels 0;
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Gonzales,M.B. and Ellis,L.
ESTs from Medicago truncatula leaves and cotyledons
Unpublished (2000)
                                                                                                                                                                                                                                                     Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
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/db xref="taxon:3880"
/clone="pDSiC-40G21"
                                                                                                                                                          Medicago truncatula
Eukaryota, Viridiplantae, Embryophyta,
Magnoliophyta, eudicotyledons, core eud
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
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                                                                                                                                                                                                                                                                                                                                  RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5" decaded with a primer [5" decaded with a primer [5" decaded with a primer [5"], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                              /...yun.com. muscurds.//db_xref=taxon:l0090"
/clone="B020032C12"
/clone_lib="RIKEN full-length enriched, 2 cells egg"
/tissue_type="egg"
/dev_stage="2 cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 286;
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                                                   /organism="Mus musculus"
                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.18;
94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 gttggatcacaagatttga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 94.79
Matches 18; Conservative
further details.
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and

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High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3687
Fax: (206) 616-3687
Email: jwallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 642 row: J column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medicago truncatula
Bukaryota, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 529)
Mahalras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gonzales, R.A., Bell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Unpublished (2000)
Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NF082E04ST1F1034 Developing stem Medicago truncatula cDNA clone NF082E04ST 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 674)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bei,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon,R.A.
                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping and
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                                                                                                                                                                         scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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/clone="Plate=642 Col=9 Row=J"
/clone_lib="RPCI-11 Human Male BAC Library"
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Pred. No. 1.8e+02;
0; Mismatches 1; Indels
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99 c 109 g 165 t
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Location/Oualiflers
1. 529
/organism="Homo sapiens"
                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW695022.1 GI:7569784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ttggatcacaagatttgat 21
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq printer: T7
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AW695022/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Strongyloides stercoralis"
/strain="Rhabditiform larvae obtained from gerbils"
/db_xref="texon:6248"
/clone_lib="TBN957#-SSR"
/lab.host="xL-1 Blue MRF" (Stratagene); Site_1:
/note="vector: Lambda Uni-24P RR (Stratagene); Site_1:
ECORI, Site_2: Xho!: mRNA was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerbils experimentally infected dogs. cDNA was constructed and, using adaptors, was cloned unidirectionally into the vector from the ECORI site to the Xho! site. The library has an unamplified titer of 1 x 10E5 pfu/ml and an amplified, undiluted titer of 9 x 10E11 pfu/ml. The average insert size of the unamplified library is 675 bp (range, 100-1700)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                  Ç
                                                                                                                                                                                                                                                                                                                   McCarter, J., Clifton, S., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colleagues of
                               BEST 16-AUG-2000 mRNA EST 16-AUG-2000 MG51cO7.y1 TBN95TM-SSR Strongyloides stercoralis cDNA 5' similar WP:T19910.2 CE16413; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L in washington out. Nematode EST Project, 1999
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Dr. Thomas Nutman and colleagues
NIAID. NIH (tnutman@hih.gov). DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 384.
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                                                                                                                                                                                                                         Strongyloides stercoralis.
Strongyloides stercoralis
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Strongyloides
                                                                                                                                                                    BE581720.1 GI:9832662
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NIH MGC http://www.ncbi.nlm.nlh.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE283043 762 bp mRNA EST 13-JUL-2000 601101323F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3493829 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin "
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                 /dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of intermodal stem segments"
119 c 133 g 203 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.1%; Score 17.4; DB 94; Length 674; 94.7%; Pred. No. 1.9e+02; 1.ve 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8541 row: n column: 06
High quality sequence stop: 661.
Location/Qualiflers
                 The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7380 Fax: 580 221 7380
                                                                                              Email: radixonenoble.org
Insert Length: 674 Std Error: 0.00
Plate: 082 row: E column: 04
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers

1 . 674
//Organism="Medicago truncatula"
//Ob_xref="taxon:3880"
                                                                                                                                                                                                                                                                 /clone="NF082E045"
/clone_lib="Developing stem"
/tissue_type="stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C2ECH II (feral)"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:3493829"
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Plant Biology Division
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Mus musculus
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Best Local Similarity
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Expressed sequence tags of CDNA clones from a C. richardii library
Unpublished (2000)
Contact: Roux SJ.
Section of Molecular Cell and Developmental Biology
University of Texas
Biology Building, Room 16, Austin, TX 78712, USA
Fax: 512 232 471 4238
                                                                                                                                                                                                                                                                                                                                                                                                                   Ceratopteris richardii.
Ceratopteris richardii
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Filicophyta;
Filicopsida; Filicales; Pteridaceae; Ceratopteris.
                                                                                                                                                                                                                                                                                                        BE642809 837 bp mRNA EST 01-SEP-2000 Cri2_7_B04_SP6 Ceratopteris Spore Library Ceratopteris richardii cDNA clone Cri2_7_B04_5', mRNA sequence.
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Pred. No. 1.96+02;
0; Mismatches 1; Indels 0;
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providing samples: Gilbert Smith, NIH"
                                                                                           Score 17.4; DB 106;
Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: sroux@uts.cc.utexas.edu
Plate: Cri2_7 row: B column:
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Best Local Similarity 94.7%;
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